



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number 115405**

**TO: James Schultz**  
**Location: REM/2D182C18**  
**Art Unit: 1635**  
**Monday, March 01, 2004**

**Case Serial Number: 09/904568**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**Remsen 1A59**  
**Phone: 571-272-2523**

**toby.port@uspto.gov**

### **Search Notes**

Dear Examiner Schultz,

Here are the results of your search.  
Please feel free to contact me if you have any questions.

Toby Port



# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor  
571-272-2507 Remsen E01 D86

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 09:53:57 ; Search time 303.726 Seconds  
(without alignments)  
9413.223 Million cell updates/sec

Title: US-09-904-568-3\_COPY\_294\_966

Perfect score: 673  
Sequence: 1 aatgctcgtcgtg9399ctg.....gtgagcgcagactgcagagac 673

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapexr 1.0

Searched: 3373863 seqs, 212409941 residues

Total number of hits satisfying chosen parameters: 3185356

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	23	3.4	48	2	AAT89912 Human ubi
C 2	22.4	3.3	36	3	AAA35922 Permutatin
C 3	21.4	3.2	43	2	AAV31116 H chain v
4	21.4	3.2	43	3	AAZ44243 Murine CD
5	21.4	3.2	50	4	AAZ44243 Murine CD
6	21.2	3.2	44	2	AAZ44243 Murine CD
7	21.2	3.2	50	4	AAZ44243 Murine CD
8	20.8	3.1	50	4	AAZ44243 Murine CD
9	20.6	3.1	40	6	ABZ49057 Human ALD
10	20.6	3.1	40	6	ABZ49057 Human ALD
11	20.6	3.1	41	2	AAZ44243 Murine CD
12	20.2	3.0	41	2	AAZ44243 Murine CD
13	20	3.0	41	2	AAZ44243 Murine CD
14	20	3.0	41	2	AAZ44243 Murine CD
15	20	3.0	41	2	AAZ44243 Murine CD
16	20	3.0	41	2	AAZ44243 Murine CD
17	19.8	2.9	45	3	AAZ44243 Murine CD
18	19.8	2.9	45	3	AAZ44243 Murine CD
19	19.8	2.9	45	3	AAZ44243 Murine CD
20	19.8	2.9	45	3	AAZ44243 Murine CD
21	19.8	2.9	45	3	AAZ44243 Murine CD
22	19.8	2.9	45	3	AAZ44243 Murine CD
23	19.6	2.9	41	6	ABZ45511 Human ATP

C 24	19.6	2.9	41	6	ABZ46917 Human ATP
C 25	19.6	2.9	45	3	AAA70390 Site dire
C 26	19.6	2.9	46	2	AAQ68290 Diabody M
C 27	19.6	2.9	48	4	ABK07023 Human NOG
C 28	19.6	2.9	50	6	AAZ44243 Murine CD
C 29	19.6	2.9	50	6	AAZ44243 Murine CD
C 30	19.4	2.9	31	2	AAZ44243 Murine CD
C 31	19.4	2.9	48	2	AAZ44243 Murine CD
C 32	19.4	2.9	48	2	AAZ44243 Murine CD
C 33	19.4	2.9	48	2	AAZ44243 Murine CD
C 34	19.4	2.9	48	2	AAZ44243 Murine CD
C 35	19.4	2.9	48	2	AAZ44243 Murine CD
C 36	19.4	2.9	48	2	AAZ44243 Murine CD
C 37	19.4	2.9	48	2	AAZ44243 Murine CD
C 38	19.4	2.9	48	2	AAZ44243 Murine CD
C 39	19.4	2.9	50	2	AAZ44243 Murine CD
C 40	19.4	2.9	50	2	AAZ44243 Murine CD
C 41	19.4	2.9	50	2	AAZ44243 Murine CD
C 42	19.4	2.9	50	2	AAZ44243 Murine CD
C 43	19.2	2.9	36	3	AAZ44243 Murine CD
C 44	19.2	2.9	47	7	ACD28216 Splicelet
C 45	19.2	2.9	50	4	AAZ44243 Murine CD

## ALIGNMENTS

RESULT 1	AAZ44243/c
ID	AAZ44243 standard; DNA; 48 BP.
XX	
AC	AAZ44243;
XX	
DT	14-APR-1998 (first entry)
XX	
DE	Human ubiquitin carrier polypeptide UbCH10 primer HSEAUC.
XX	
KW	Ubiquitin carrier protein; UbCH10; human; cyclin A; cyclin B;
KM	Ubiquitination; cell cycle; mitosis; PCR; primer; AUI epitope;
KX	dominant negative mutant; ss.
XX	
OS	Synthetic.
XX	
XX	Homo sapiens.
XX	
PN	MO9737027-A1.
XX	
PD	09-OCT-1997.
XX	
PF	31-MAR-1997; 97WO-US005296.
XX	
PR	01-APR-1996; 96US-0014492P.
PR	18-MAR-1997; 97US-00820639.
PR	31-MAR-1997; 97US-00828533.
XX	
PA	(HARD) HARVARD COLLEGE.
XX	
XX	Rudderman JV, Hershko A, Kirschner MW, Townsley F, Aristarkov A;
PI	Eylan E, Yu H;
XX	
DR	WPI; 1997-503112/46.
XX	
PT	New ubiquitin carrier polypeptide(s) - are involved in ubiquitination of
PT	cyclin A and cyclin B and are useful to screen for new inhibitors of cell
PT	proliferation.
XX	
PS	Example 8; Page 86; 138pp; English.
XX	
CC	PCR antisense primer HSEAUC (AAZ44243) encodes the last 6 amino acids of
CC	the open reading frame (HSEAUC) of UbCH10 (see AAZ44243), a novel
CC	human ubiquitin carrier protein that is involved in the ubiquitination
CC	and degradation of mitotic cyclins. HSEAUC also encodes the amino acids
CC	DIYRI (AUI epitope) and includes 2 stop codons and an HindIII
CC	restriction site. It was used with sense primer HSEN (see AAT89910) to

CC add the AVI epitope to the C-terminus of wild-type UbcH10 and its  
CC Cys14Ser mutant (see AAW31279). Tagged proteins were expressed in E.  
CC coli and used in tests to examine the in vivo and in vitro activity of  
CC UbcH10 and its dominant negative mutant  
XX  
SQ Sequence 48 BP; 9 A; 9 C; 17 G; 13 T; 0 U; 0 Other;  
Query Match 3.4%; Score 23; DB 2; Length 48;  
Best Local Similarity 83.9%; Pred. No. 5.1e+04;  
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 304 CACCGACCTGAAGCCTGACACCTTACAGGAC 334  
DB 47 CACCGACCGAGAGCCCGACCTACAGGTAC 17  
RESULT 2  
ID AAW35922/c  
AAW35922 standard; DNA; 36 BP.  
XX  
XX AAA35922;  
AC  
XX  
XX 26-JUL-2000 (first entry)  
DT  
XX  
XX Permutin linker encoding nucleotide sequence RGS152.  
DE  
XX  
XX Biologically-activated circularly-permuted protein; permutin; linker;  
KW permutin library generation; therapeutic property; antigen;  
KW immunotherapy; improve bio-distribution; half life; ss.  
XX  
XX Synthetic.  
OS  
XX WO200018905-A1.  
PN  
XX  
XX 06-APR-2000.  
PD  
XX  
XX 24-SEP-1999; 99WO-US020891.  
PF  
XX  
XX 25-SEP-1998; 98US-0101908P.  
PR  
XX  
XX (SEAR) SEARLE & CO G. D.  
PA  
XX  
XX Lee SC;  
PI  
XX  
XX WPI; 2000-293145/25.  
DR  
XX  
XX Preparation of biologically-activated circularly-permuted proteins by  
PT scanning permutagenesis for generating libraries of permutins with  
PT improved therapeutic properties.  
XX  
XX  
XX Claim 11; Page 44; 100pp; English.  
XX  
XX The preparation of biologically-activated circularly-permuted proteins  
CC (permutins) comprises the use of a method comprising making a series of  
CC circularly permuted genes. The circularly permuted genes are inserted  
CC into a display vector, where they are expressed so that the proteins they  
CC encode are presented on the surface of the display vector. A library of  
CC display vectors presenting the expressed circularly permuted proteins is  
CC generated. A target protein that can bind a biologically active  
CC circularly permuted protein can be used to affinity select the presenting  
CC display vectors. The selected display vectors can be isolated and  
CC analyzed to identify the presented circularly-permuted protein. The  
CC permutins conform to the structure of a parent protein consisting of a  
CC segment derived from the carboxy portion of the parent protein, a segment  
CC derived from the amino terminus of the parent protein, and a linker or  
CC chemical bond linking the amino and carboxy terminal derived portions.  
CC Nucleotide sequences AAW3576-A35943 encode linkers used to create the  
CC permutins of the invention. The method is used to generate libraries of  
CC permutins with improved therapeutic properties compared to their parent  
CC molecules. Permutins with little or no activity may be used as antigens  
CC for producing antibodies which are used in immunology or immunotherapy as  
CC probes or intermediates used to construct other useful permutins.  
CC Permutins have improved biological and therapeutic properties compared

CC to their two individual components due to alterations in bio-distribution  
CC or half-life  
XX  
SQ Sequence 36 BP; 5 A; 15 C; 10 G; 6 T; 0 U; 0 Other;  
Query Match 3.3%; Score 22.4; DB 3; Length 36;  
Best Local Similarity 81.2%; Pred. No. 6.6e+04;  
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 425 GCCCGAGCAGCGGGGCTGCTGCCGATGT 456  
DB 35 GCCCGAGCAGCGGGGCTGCTGCCGATAT 4  
RESULT 3  
ID AAV31116  
AAV31116 standard; DNA; 43 BP.  
XX  
XX AAV31116;  
AC  
XX  
XX 02-SEP-1998 (first entry)  
DT  
XX  
XX H chain variable region from mouse anti-MY-10 PCR primer 1.  
DE  
XX  
XX Mouse; anti-MY-10; H chain variable region; L chain variable region;  
KW antibody; heavy; light; CDR; human CD34 antigen; hybridoma; anti-CD34;  
KW PCR primer; ss.  
XX  
XX Synthetic.  
OS  
XX JP10155489-A.  
PN  
XX  
XX 16-JUN-1998.  
PD  
XX  
XX 27-NOV-1996; 96JP-00331647.  
PF  
XX  
XX 27-NOV-1996; 96JP-00331647.  
PR  
XX  
XX (ASAH) ASAH KASEI KOGYO KK.  
PA (ASAH) ASAH MEDICAL CO LTD.  
XX  
XX WPI; 1998-391043/34.  
DR  
XX  
XX Recombinant antibody against human CD34 - and nucleic acid encoding it,  
PT used for efficient production of the antibody.  
PT  
XX  
XX Example 4; Page 7; 15pp; Japanese.  
XX  
XX The present invention describes a nucleic acid which encodes an anti-MY-  
CC 10 antibody. The present sequence represents a PCR primer for the H chain  
CC variable region of the antibody. Also described is a method for the  
CC production of a recombinant antibody in which the above nucleic acid is  
CC used to produce an antibody which combines with human CD34 antigen by  
CC gene recombination. The anti-CD34 antibody gene is used to produce  
CC recombinant anti-CD34 antibodies efficiently, which can be used in  
CC pharmaceuticals  
XX  
SQ Sequence 43 BP; 8 A; 15 C; 16 G; 4 T; 0 U; 0 Other;  
Query Match 3.2%; Score 21.4; DB 2; Length 43;  
Best Local Similarity 71.8%; Pred. No. 1.2e+05;  
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 513 CCTGACCGCAGCGCTCTGATGCACTGAAGCTTTAG 551  
DB 5 CCTGACCGCAGCGCTCTGATGCACTGAAGCAGTCAG 43  
RESULT 4  
ID AAZ44243  
AAZ44243 standard; DNA; 43 BP.  
XX



AC AA244243;  
 XX  
 DT 31-MAR-2000 (first entry)  
 XX  
 DE Murine CD4/CD34 recognizing antibody primer 7.  
 XX  
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine; primer; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9961629-A1.  
 XX  
 PD 02-DEC-1999.  
 XX  
 PF 24-MAY-1999; 99WO-JP002711.  
 XX  
 PR 25-MAY-1998; 98JP-00159957.  
 PR 26-MAY-1998; 98JP-00163023.  
 XX  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 PA (ASAH ) ASAH MEDICAL CO LTD.  
 XX  
 PI Ono M, Soka T, Morimoto I, Miyamura K;  
 XX  
 DR WPI, 2000-086720/07.  
 XX  
 PT Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells.  
 XX  
 PS Example 21; Page 54; 11pp; Japanese.  
 XX  
 CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for the  
 CC collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal compositions  
 CC for the treatment of HIV infection and autoimmune diseases. AA244237-  
 CC Z44246 represent primers used to illustrate the method of the invention  
 CC  
 SO Sequence 43 BP; 8 A; 15 C; 16 G; 4 T; 0 U; 0 Other;  
 XX  
 QY Query Match 3.2%; Score 21.4; DB 3; Length 43;  
 Best Local Similarity 71.8%; Pred. No. 1.2e+05;  
 Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 XX  
 Db 513 CCGTCGACCCGAGCGTCTGATGACGCTGAAGCTTTTCAG 551  
 5 CCGAGCCGCGCCATGCGCCGAGTGCAGTGAAGCAGTCAAG 43  
 XX  
 RESULT 5  
 AA128467  
 ID AA128467 standard; DNA; 50 BP.  
 XX  
 AC AA128467;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Human SNP oligonucleotide #1675.  
 XX  
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinase; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 XX

OS Homo sapiens.  
 XX  
 PN WO200147944-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US035498.  
 XX  
 PR 28-DEC-1999; 99US-0173419P.  
 PR 27-DEC-2000; 2000US-00173419.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shimkets RA, Leach M;  
 XX  
 DR WPI, 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.  
 XX  
 PS Claim 1; Page 1859; 4143pp; English.  
 XX  
 CC The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinases, cytokines, interferons, interleukins, G-  
 CC protein coupled receptors and thioesterases. The present sequence is one  
 CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate expression of the proteins listed above.  
 CC Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms  
 CC  
 SO Sequence 50 BP; 9 A; 14 C; 22 G; 5 T; 0 U; 0 Other;  
 XX  
 QY Query Match 3.2%; Score 21.4; DB 4; Length 50;  
 Best Local Similarity 66.0%; Pred. No. 1.2e+05;  
 Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
 XX  
 Db 56 AGTGGCGAGTGAGTTTCTTGCGGCGCCGAGCTTCTCCAGAGGTGAC 102  
 2 AGGGGAGAGCTGGGAGTGGGAGGCCCATCTGCCCCAGAGGTGGC 48  
 XX  
 RESULT 6  
 AA119291/c  
 ID AA119291 standard; DNA; 44 BP.  
 XX  
 AC AA119291;  
 XX  
 DT 17-MAY-1999 (first entry)  
 XX  
 DE Human granulocyte colony-stimulating factor antisense primer oligo 1.  
 XX  
 KW Human; granulocyte colony-stimulating factor; G-CSF; hG-CSF;  
 KW haematopoiesis disorder; primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9853072-A1.  
 XX  
 PR 26-NOV-1998.  
 XX  
 PF 21-MAY-1998; 98WO-KR000125.  
 XX



PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
XX autoimmune diseases and infections.  
XX Claim 1, Page 33:5, 4143pp; English.  
XX The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.  
CC Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms  
XX  
SQ Sequence 50 BP; 7 A; 11 C; 23 G; 9 T; 0 U; 0 Other;  
Query Match 3.1%; Score 20.8; DB 4; Length 50;  
Best Local Similarity 70.0%; Pred. No. 1.7e+05;  
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
QY 73 CTTGGGGGCCCGCTTCTCCAGAGGTGGCAGCANTGSCC 112  
DB 7 CGTGGGGCTCAGGGGGTCCATAGGCGAGCAGACTGGTC 46  
RESULT 9  
ABZ49057/C  
ID ABZ49057 standard; DNA; 40 BP.  
XX  
XX ABZ49057;  
AC  
XX  
XX 26-JUN-2003 (first entry)  
DT  
XX  
XX Human ALDH1L1/FTHPD gene polymorphic site, #5840.  
DE  
XX  
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 3;  
KM polymorphic site; drug evaluation; drug screening; genotyping;  
KM genetic profiling; therapeutic customisation; adverse reaction;  
KM clinical trial; drug approval; ds.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH variation replace(20..21,CCT)  
FT /\*tag= a  
XX  
XX WO200252044-A2.  
XX  
XX 04-JUL-2002.  
PD  
XX  
XX 27-DEC-2001; 2001WO-JP011592.  
PF  
XX  
XX 27-DEC-2000; 2000JP-00399443.  
PR  
XX 02-MAY-2001; 2001JP-00135256.  
PR  
XX 27-AUG-2001; 2001JP-00256862.  
XX  
XX (RIKE ) RIKEN KK.  
XX  
XX Nakamura Y, Sekine A, Iida A, Satto S;  
PI  
XX WPI; 2002-583571/62.  
DR  
XX  
XX Identifying individuals having a polymorphism, useful for determining the  
PT effectiveness or side effect of a drug or treatment protocol, comprises  
PT detecting at least one polymorphism in the drug metabolizing enzyme

PT nucleic acid.  
XX  
XX Claim 23, Page 180; 2785pp; English.  
XX  
XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
CC encoding enzymes associated with drug metabolism. The invention relates  
CC to methods and compositions for identifying individuals who have at least  
CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
CC polymorphisms may be identified in a nucleic acid sample using probes or  
CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
CC variety of detection assays, including hybridisation assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC polymorphism data, particularly that relating to single nucleotide  
CC polymorphisms (SNPs), may be used in studying the relationship between  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolising enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to an increase in the range of  
CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy  
XX  
SQ Sequence 40 BP; 6 A; 15 C; 9 G; 10 T; 0 U; 0 Other;  
Query Match 3.1%; Score 20.6; DB 6; Length 40;  
Best Local Similarity 74.3%; Pred. No. 1.8e+05;  
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 133 CAGGAGCAGCTTCAGAAAGTTGCTGAAGTTGGG 167  
DB 36 CAGCAGCAGCTCGAGAGTAGCTGCAGATTGGG 2  
RESULT 10  
ABZ46527/C  
ID ABZ46527 standard; DNA; 40 BP.  
XX  
XX ABZ46527;  
AC  
XX  
XX 26-JUN-2003 (first entry)  
DT  
XX  
XX Human ALDH1L1/FTHPD gene polymorphic site, #3311.  
DE  
XX  
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 3;  
KM polymorphic site; drug evaluation; drug screening; genotyping;  
KM genetic profiling; therapeutic customisation; adverse reaction;  
KM clinical trial; drug approval; ds.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH variation replace(20..21,CCT)  
FT /\*tag= a  
XX  
XX WO200252044-A2.  
XX  
XX 04-JUL-2002.  
PD





PD 04-JUL-2002.

XX 27-DEC-2001; 2001WO-JP011592.

XX 27-DEC-2000; 2000JP-00399443.

PR 02-MAY-2001; 2001JP-00135256.

PR 27-AUG-2001; 2001JP-00256862.

XX (RIKE ) RIKEN KK.

XX Nakamura Y, Sekine A, Iida A, Saito S;

PI WPI; 2002-583571/62.

DR Identifying individuals having a polymorphism, useful for determining the

XX effectiveness or side effect of a drug or treatment protocol, comprises

PT detecting at least one polymorphism in the drug metabolizing enzyme

PT nucleic acid.

XX Claim 23; Page 66; 2785pp; English.

XX Sequences AB243217-AB250887 represent polymorphic sites within genes

CC encoding enzymes associated with drug metabolism. The invention relates

CC to methods and compositions for identifying individuals who have at least

CC one polymorphism in such drug metabolizing enzyme-encoding genes. The

CC polymorphisms may be identified in a nucleic acid sample using probes or

CC primers specific for a sequence selected from AB243217-AB250887, using a

CC variety of detection assays, including hybridisation assays, nucleic acid

CC arrays and PCR-based methods. The invention also encompasses methods of

CC evaluating and screening drugs using genetic polymorphism data. Genetic

CC polymorphism data, particularly that relating to single nucleotide

CC polymorphisms (SNPs), may be used in studying the relationship between

CC DNA sequence variations and human diseases, conditions, and responses to

CC drugs. SNPs are also useful as polymorphism markers for discovering genes

CC that cause or exacerbate certain diseases. SNPs are particularly useful

CC in the above respects as they are stable in populations, occur

CC frequently, and have lower mutation rates than other genome variations

CC such as repeating sequences. The detection and analysis of polymorphisms

CC in genes encoding drug metabolising enzymes allows the customisation of

CC drug therapies based upon the genetic profile of individual patients.

CC This would not only take the guesswork out of selecting the drug with the

CC greatest therapeutic effect for a particular patient, but would also

CC reduce the likelihood of adverse reactions, thereby increasing safety.

CC Methods of the invention are also useful in the drug discovery and

CC approval processes. For example, individuals could be selected for

CC clinical trials only if their genetic profiles indicate that they are

CC capable of responding to a particular drug or drug class, and previously

CC failed drug candidates could be revived if they were matched with more

CC appropriate patient populations. The methods, data and compositions of

CC the invention may therefore lead to an increase in the range of

CC possible drug targets and decreases in the number of adverse drug

CC reactions, failed drug trials, the time taken for a drug to be approved,

CC the length of time patients are on medication and the number of different

CC medications a patient needs to take before finding an effective therapy

XX SQ Sequence 41 BP; 6 A; 15 C; 14 G; 6 T; 0 U; 0 Other;

Query Match 3.0%; Score 20; DB 6; Length 41;

Best Local Similarity 72.2%; Pred. No. 2.5e-05;

Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 339 TCAGAGCTCTGCTCCCTCCAGACCTGCTGGG 374

DB 2 TGCAGGCGCCTGCTCCCTCCAGACCTGCTGGG 37

RESULT 15

ABT34022/c

ID ABT34022 standard; DNA; 45 BP.

XX AC ABT34022;

XX 29-MAY-2003 (first entry)

DT

XX Human pigmentation trait-related PCR primer - SEQ ID No 121.

XX Human; single nucleotide polymorphism; SNP; ss; melanocortin-1 receptor;

KW genetic pigmentation trait; MC1R; agouti signaling protein; ASIP; race;

KW hair colour; eye colour; forensic tool; PCR; primer.

XX Homo sapiens.

XX WO200297047-A2.

XX 05-DEC-2002.

XX 28-MAY-2002; 2002WO-US016789.

XX 25-MAY-2001; 2001US-0293560P.

PR 21-JUN-2001; 2001US-0300187P.

PR 07-AUG-2001; 2001US-0310781P.

PR 17-SEP-2001; 2001US-0323662P.

PR 26-OCT-2001; 2001US-0344419P.

PR 15-NOV-2001; 2001US-0334674P.

PR 02-JAN-2002; 2002US-0346303P.

XX (DNAP-) DNAPRINT GENOMICS INC.

PA Frudakis T;

PI WPI; 2003-239091/23.

XX Inferring genetic pigmentation trait such as hair/eye color or shade from

XX nucleic acid sample of human subject, by identifying a pigmentation-

XX related haplotype allele of a pigmentation gene in the sample.

XX Example 17; Page 245; 396pp; English.

XX The invention comprises a method for inferring a genetic pigmentation

XX trait of a human. The method involves identifying a single nucleotide

XX polymorphism (SNP) in a pigmentation gene - where the pigmentation gene

XX is not melanocortin-1 receptor (MC1R) and agouti signaling protein

XX (ASIP). The method of the invention is useful for inferring a genetic

XX pigmentation trait of a human, especially for inferring the race of a

XX human subject. The method is useful for inferring a genetic pigmentation

XX trait such as hair shade or colour, or eye shade or colour of a human

XX subject. The method may be used as a forensic tool for obtaining

XX information relating to physical characteristics of a potential crime

XX victim or a perpetrator of a crime from a nucleic acid sample present at

XX a crime scene. The present PCR primer is used in the exemplification of

XX the invention

XX SQ Sequence 45 BP; 13 A; 12 C; 15 G; 5 T; 0 U; 0 Other;

Query Match 3.0%; Score 20; DB 7; Length 45;

Best Local Similarity 72.2%; Pred. No. 2.5e+05;

Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 72 TCTTGGGGGCCAGCTTCTCTCCAGAGGTGGCAGCAA 107

DB 44 TCTTGGGGGCCAGCTTCTCTCCAGAGGTGGCAGCAA 9

Search completed: February 29, 2004, 12:01:11

Job time : 308.726 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 11:48:29 ; Search time 67.9494 Seconds  
(without alignments)  
5488.301 Million cell updates/sec

Title: US-09-904-568-1\_COPY\_132\_803  
Perfect score: 672  
Sequence: 1 agctctgtttgggggctgc.....gtgagcgcaactgcaggac 672

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 839752

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21.2	3.2	47	4	US-09-671-317-808
C 2	20.6	3.1	47	4	US-08-671-317-639
C 3	20.2	3.0	35	4	US-09-514-247A-2
C 4	20	3.0	50	1	US-08-171-389-463
C 5	20	3.0	50	1	US-08-123-936-463
C 6	20	3.0	50	2	US-08-475-228A-463
C 7	20	3.0	50	3	US-08-482-080A-463
C 8	20	3.0	50	4	US-09-354-947-463
C 9	20	3.0	50	5	PCT-US93-12388-463
C 10	19.8	2.9	46	3	US-09-252-292-22
C 11	19.2	2.9	44	3	US-08-617-785-19
C 12	19.2	2.9	44	4	US-09-817-464-19
C 13	19.2	2.9	47	4	US-09-422-978-2676
C 14	19	2.8	27	2	US-08-859-998-80
C 15	19	2.8	27	4	US-09-325-928-80
C 16	19	2.8	27	4	US-09-325-2018-80
C 17	18.6	2.8	43	3	US-09-392-071-15
C 18	18.6	2.8	43	3	US-08-732-708C-6
C 19	18.6	2.8	43	3	US-09-292-069A-15
C 20	18.6	2.8	43	3	US-09-418-721-15
C 21	18.6	2.8	43	4	US-09-767-013-15
C 22	18.6	2.8	43	4	US-09-292-072-15
C 23	18.4	2.7	31	4	US-09-556-601-17
C 24	18.4	2.7	37	1	US-08-428-733A-7
C 25	18.4	2.7	37	1	US-08-428-733A-39
C 26	18.4	2.7	47	1	US-08-336-132-22
C 27	18.2	2.7	27	4	US-09-870-956-48

C 28	18.2	2.7	45	1	US-08-176-412-5
C 29	18.2	2.7	45	2	US-08-555-268A-5
C 30	18.2	2.7	45	2	US-08-495-695B-5
C 31	18.2	2.7	45	5	PCT-US94-1436-5
C 32	18.2	2.7	47	1	US-08-171-389-74
C 33	18.2	2.7	47	1	US-08-123-936-74
C 34	18.2	2.7	47	2	US-08-475-228A-74
C 35	18.2	2.7	47	3	US-08-482-080A-74
C 36	18.2	2.7	47	4	US-09-354-947-74
C 37	18.2	2.7	47	4	US-09-671-317-788
C 38	18.2	2.7	47	5	PCT-US93-12388-74
C 39	18	2.7	39	3	US-09-262-773-78
C 40	18	2.7	47	4	US-09-671-317-839
C 41	18	2.7	47	4	US-08-422-978-1159
C 42	18	2.7	50	2	US-08-989-394-12
C 43	18	2.7	50	3	US-09-271-365-12
C 44	18	2.7	50	4	US-09-604-013A-12
C 45	17.8	2.6	40	1	US-08-195-874-4

ALIGNMENTS

RESULT 1  
US-09-671-317-808/c  
; Sequence 808, Application US/09671317  
; Patent No. 6528260  
; GENERAL INFORMATION:  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Cohen, Annick  
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM  
; FILE REFERENCE: 62.US3.CIP  
; CURRENT APPLICATION NUMBER: US/09/671,317  
; CURRENT FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US 09/536,178  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT/IB00/00403  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: US 60/126,269  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: US 60/131,961  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 977  
; SOFTWARE: Patent.pm  
; SEQ ID NO 808  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 24  
; OTHER INFORMATION: 12-132-437 : polymorphic base A or C  
US-09-671-317-808

Query Match 3.2%; Score 21.2; DB 4; Length 47;  
Best Local Similarity 65.9%; Pred. No. 2.3e+03;  
Matches 29; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 96 AGTACGCGCCGTGCTCAGCTTGAAGGACTTAGACAGGAGCA 139  
DB 44 AGCGATGCCCTTGGGGCAGAKTTGGAGGAGGGGACAGGAGCA 1

RESULT 2  
US-09-671-317-639  
; Sequence 639, Application US/09671317  
; Patent No. 6528260  
; GENERAL INFORMATION:  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; APPLICANT: Bougueleret, Lydie

US-08-171-389-463/c  
; Sequence 463, Application US/08171389  
; Patent No. 5578444

GENERAL INFORMATION:  
APPLICANT: Edwards, Cynthia A.  
APPLICANT: Cantor, Charles R.

GENERAL INFORMATION:  
APPLICANT: Edwards, Cynthia A.  
APPLICANT: Cantor, Charles R.



APPLICANT: Andrews, Beth M.  
APPLICANT: Turin, Lisa M.  
TITLE OF INVENTION: Screening Assay for the Detection of  
DNA-Binding Molecules  
NUMBER OF SEQUENCES: 640  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genelabs Technologies, Inc.  
STREET: 505 Penobscot Drive  
CITY: Redwood City  
STATE: CA  
COUNTRY: USA  
ZIP: 94063  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/123,936  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/996,783  
FILING DATE: 23-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/723,618  
FILING DATE: 27-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 463:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Human insulin-like growth factor II  
INDIVIDUAL ISOLATE: gene  
US-08-123-936-463

Query Match 3.0%; Score 20; DB 1; Length 50;  
Best Local Similarity 65.9%; Pred. No. 5.5e+03;  
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 259 GCGGGCACACACCTGTCTCCAGCAGGCTCTCCGGCTGCCCC 302  
Db 49 GCGGGCGCCACGCCCGCTCTTATAGTCGGCGCAGCGCGGC 6

RESULT 6  
US-08-475-228A-463/c  
Sequence 463, Application US/08475228A  
Patent No. 5869241  
GENERAL INFORMATION:  
APPLICANT: Edwards, Cynthia A.  
APPLICANT: Cantor, Charles R.  
APPLICANT: Andrews, Beth M.  
APPLICANT: Turin, Lisa M.  
APPLICANT: Fry, Kirk E.  
TITLE OF INVENTION: Sequence-Directed DNA Binding  
NUMBER OF SEQUENCES: 664  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genelabs Technologies, Inc.  
STREET: 505 Penobscot Drive  
CITY: Redwood City

STATE: CA  
COUNTRY: USA  
ZIP: 94063  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,228A  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/123,936  
FILING DATE: 17-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/996,783  
FILING DATE: 23-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/723,618  
FILING DATE: 27-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/081,070  
FILING DATE: 22-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 463:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Human insulin-like growth factor II  
INDIVIDUAL ISOLATE: gene  
US-08-475-228A-463

Query Match 3.0%; Score 20; DB 2; Length 50;  
Best Local Similarity 65.9%; Pred. No. 5.5e+03;  
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 259 GCGGGCACACACCTGTCTCCAGCAGGCTCTCCGGCTGCCCC 302  
Db 49 GCGGGCGCCACGCCCGCTCTTATAGTCGGCGCAGCGCGGC 6

RESULT 7  
US-08-482-080A-463/c  
Sequence 463, Application US/08482080A  
Patent No. 6010849  
GENERAL INFORMATION:  
APPLICANT: Edwards, Cynthia A.  
APPLICANT: Cantor, Charles R.  
APPLICANT: Andrews, Beth M.  
APPLICANT: Turin, Lisa M.  
APPLICANT: Fry, Kirk E.  
TITLE OF INVENTION: Sequence-Directed DNA Binding  
NUMBER OF SEQUENCES: 664  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genelabs Technologies, Inc.  
STREET: 505 Penobscot Drive  
CITY: Redwood City  
STATE: CA  
COUNTRY: USA  
ZIP: 94063  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,080A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,080  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/171,389  
FILING DATE: 20-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/123,936  
FILING DATE: 17-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/996,783  
FILING DATE: 23-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/723,618  
FILING DATE: 27-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/081,070  
FILING DATE: 22-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Brady, John F.  
REGISTRATION NUMBER: 39,118  
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 324-0880  
TELEFAX: (650) 324-0960  
INFORMATION FOR SEQ ID NO: 463:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Human insulin-like growth factor II  
INDIVIDUAL ISOLATE: gene  
US-08-482-080A-463

Query Match 3.0%; Score 20; DB 3; Length 50;  
Best Local Similarity 65.9%; Pred. No. 5.5e+03;  
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 259 GCGGCGCACACACACCTGCTCCAGCAGGCTCTCCGGGTGCCCC 302  
Db 49 GCGGCGGCCACCGCCGGCTCTTATAGTCGCGCCAGCGCGGCC 6

## RESULT 8

US-09-354-947-463/c  
Sequence 463, Application US/09354947  
Patent No. 6384208  
GENERAL INFORMATION:

APPLICANT: Edwards, Cynthia A.  
APPLICANT: Cantor, Charles R.  
APPLICANT: Andrews, Beth M.  
APPLICANT: Turin, Lisa M.  
APPLICANT: Fy, Kirk E.  
TITLE OF INVENTION: Sequence-Directed DNA Binding  
TITLE OF INVENTION: Molecules, Compositions and Methods  
NUMBER OF SEQUENCES: 664  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genelabs Technologies, Inc.  
STREET: 505 Penobscot Drive  
CITY: Redwood City  
STATE: CA  
COUNTRY: USA  
ZIP: 94063  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,947  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,080  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/171,389  
FILING DATE: 20-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/123,936  
FILING DATE: 17-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/996,783  
FILING DATE: 23-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/723,618  
FILING DATE: 27-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/081,070  
FILING DATE: 22-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Brady, John F.  
REGISTRATION NUMBER: 39,118  
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 324-0880  
TELEFAX: (650) 324-0960  
INFORMATION FOR SEQ ID NO: 463:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Human insulin-like growth factor II  
INDIVIDUAL ISOLATE: gene  
US-09-354-947-463

Query Match 3.0%; Score 20; DB 4; Length 50;  
Best Local Similarity 65.9%; Pred. No. 5.5e+03;  
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 259 GCGGCGCACACACACCTGCTCCAGCAGGCTCTCCGGGTGCCCC 302  
Db 49 GCGGCGGCCACCGCCGGCTCTTATAGTCGCGCCAGCGCGGCC 6

## RESULT 9

PCT-US93-12388-463/c  
Sequence 463, Application PC/TUS9312388  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: Sequence-Directed DNA Binding  
TITLE OF INVENTION: Molecules, Compositions and Methods  
NUMBER OF SEQUENCES: 641  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genelabs Technologies, Inc.  
STREET: 505 Penobscot Drive  
CITY: Redwood City  
STATE: CA  
COUNTRY: USA  
ZIP: 94063  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/12388

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/123,936

FILING DATE: 17-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/996,783

FILING DATE: 23-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 463:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Human insulin-like growth factor II

INDIVIDUAL ISOLATE: gene

PCT-US93-12388-463

Query Match

Best Local Similarity 3.0%; Score 20; DB 5; Length 50;

Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 259 GGGGCGCCACACACCGCTCTCCAGCAGCGCTCTCCGGCTGCCCCC 302

DB 49 GGGGCGCCACACCGCGCTCTTATAGTCGCCAGCGCGGCC 6

RESULT 10

US-09-252-292-22

Sequence 22, Application US/0925292B

Patent No. 6245968

GENERAL INFORMATION:

APPLICANT: Boudec, Philippe

APPLICANT: Rodgers, Matthew

APPLICANT: Dumas, Florence

TITLE OF INVENTION: Mutated hydroxyphenylpyruvate dioxygenase, DNA

TITLE OF INVENTION: sequence and isolation of plants which contain such a

FILE REFERENCE: 5500731

CURRENT APPLICATION NUMBER: US/09/252,292B

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 08/982,772

PRIOR FILING DATE: 1997-12-02

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 22

LENGTH: 46

TYPE: DNA

ORGANISM: Plant

US-09-252-292-22

Query Match

Best Local Similarity 2.9%; Score 19.8; DB 3; Length 46;

Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 550 GATGACTGACACACCGCTTCGAGTGCCCATAGCCAAA 588

DB 4 GATGACTGACACACCGCTTCGAGTGCCCATAGCCAAA 42

RESULT 11

US-08-617-785-19/c

Sequence 19, Application US/08617785E

Patent No. 6228610

GENERAL INFORMATION:

APPLICANT: Flor, Peter J.

APPLICANT: Kuhn, Ranier

APPLICANT: Lindaur, Kristen

APPLICANT: Puttnar, Irene

APPLICANT: Knopfel, Thomas

TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,

FILE REFERENCE: 4-19679/A/PCT

CURRENT APPLICATION NUMBER: US/08/617,785E

EARLIER FILING DATE: 1996-03-19

EARLIER APPLICATION NUMBER: PCT/EP94/02991

EARLIER FILING DATE: 1994-09-07

EARLIER APPLICATION NUMBER: EPO 9416553.7

EARLIER FILING DATE: 1994-08-19

EARLIER APPLICATION NUMBER: EPO 93810663.0

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 19

LENGTH: 44

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION:

OTHER INFORMATION: Oligonucleotide primer

US-09-617-464-19

Query Match

Best Local Similarity 2.9%; Score 19.2; DB 4; Length 44;

Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 266 CACACACCTGCTCCAGCAGCGCTCTCCGCTGCCCTCCCTGC 305

DB 42 CCGGCTCTAGCCCTAGCAGCGCCCTCGCGCCCTCGCAGC 3

RESULT 12

US-09-817-464-19/c

Sequence 19, Application US/09817464

Patent No. 6515107

GENERAL INFORMATION:

APPLICANT: Flor, Peter J.

APPLICANT: Kuhn, Ranier

APPLICANT: Lindaur, Kristen

APPLICANT: Puttnar, Irene

APPLICANT: Knopfel, Thomas

TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,

FILE REFERENCE: 4-19679/A/PCT

CURRENT APPLICATION NUMBER: US/09/817,464

EARLIER FILING DATE: 2001-03-26

EARLIER APPLICATION NUMBER: US/08/617,785

EARLIER FILING DATE: 1996-03-19

EARLIER APPLICATION NUMBER: EPO 9416553.7

EARLIER FILING DATE: 1994-08-19

EARLIER APPLICATION NUMBER: EPO 93810663.0

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 19

LENGTH: 44

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION:

OTHER INFORMATION: Oligonucleotide primer

US-09-817-464-19

```
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 266 CACACACCTGTCAGAGGCTCTCCGGCTGCCCTGC 305
Db 42 CCGGTCCTAGCCCTAGCAGGCGCTCGGCGCCCTGCAGC 3

RESULT 13
US-09-422-978-2676
; Sequence 2676, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 2676
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-13864-64 : polymorphic base G or T
US-09-422-978-2676

Query Match 2.9%; Score 19.2; DB 4; Length 47;
Best Local Similarity 70.6%; Pred. No. 9.5e+03;
Matches 24; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 272 CCTGCTCAGCAGGCTCTCCGGCTGCCCTGC 305
Db 10 CCTCTCCACAGCTGCCCTCTCCCTGC 43

RESULT 14
US-08-859-998-80/c
; Sequence 80, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jekhade, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
```

```
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-80

Query Match 2.8%; Score 19; DB 2; Length 27;
Best Local Similarity 81.5%; Pred. No. 8.3e+03;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 43 GCTGACAGTCACAGTGCGCGGTCAGT 69
Db 27 GCAGACAGTCACACTGCTTTGGTCAGT 1

RESULT 15
US-09-225-328-80/c
; Sequence 80, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jekhade, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
```



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: February 29, 2004, 09:53:57 ; Search time 303.274 Seconds  
(without alignments)  
9413.223 Million cell updates/sec

Title: US-09-904-568-1\_COPY\_132\_803  
Perfect score: 672  
Sequence: 1 agtgtctttggggcgc.....gtgagcgcaactgcagcagc 672

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 3185356

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	21.8	3.2	49	6	ABA99919 Human TNF
C 2	21.4	3.2	50	7	ABZ24835 Herpes S1
C 3	21.1	3.1	30	3	AAA71444 Human meg
C 4	21.1	3.1	33	6	ABL40388 Primer 3
C 5	21.1	3.1	40	2	AAT89030 Solid pha
C 6	20.8	3.1	42	2	AAQ52858 Cytomegal
C 7	20.8	3.1	49	2	AAT80503 Hepatoma
C 8	20.2	3.0	35	2	AAT7583 PPAR CNNA
C 9	20.2	3.0	41	4	AAI66427 Kringle p
C 10	20.2	3.0	44	2	AAQ22113 S3 chimera
C 11	20.2	3.0	50	4	AAI34545 Human SNP
C 12	20.2	3.0	50	2	AAQ69713 Human ins
C 13	20.2	3.0	50	2	AAT64175 Human ins
C 14	20.2	3.0	50	2	AAI17463 Test sequ
C 15	20.2	3.0	50	6	ABK2954 DNA bindi
C 16	20.2	3.0	50	6	ABZ00686 Human leu
C 17	20.2	3.0	50	10	AD80493 Duplex ol
C 18	19.6	2.9	40	7	ACA55333 Human mod
C 19	19.6	2.9	47	3	AZ68329 Human map
C 20	19.6	2.9	50	8	ACD17187 Mouse ant
C 21	19.4	2.9	41	6	ABZ43700 Human HNK
C 22	19.4	2.9	41	6	ABZ49884 Human HNK
C 23	19.4	2.9	41	6	ABV75966 Human ATP

24	19.4	2.9	50	4	AAH89679	Aah89679 Human rib
C 25	19.4	2.9	50	6	ABZ00318	Abz00318 Human leu
C 26	19.2	2.9	32	2	AAV90578	Aav90578 Reverse p
C 27	19.2	2.9	33	6	ABK96448	Abk96448 PCR prime
C 28	19.2	2.9	50	4	AAI29231	Aai29231 Human SNP
C 29	19.2	2.9	50	6	ABZ01371	Abz01371 Human leu
C 30	19.2	2.9	50	6	ABZ01296	Abz01296 Human leu
C 31	19.2	2.9	50	6	ABK65992	Abk65992 Human gen
C 32	19.2	2.8	27	6	ABQ82800	Abq82800 Human Akt
C 33	19.2	2.8	33	7	ABV76886	Abv76886 3' PCR pr
C 34	19.2	2.8	33	7	ABQ82813	Abq82813 Human Akt
C 35	19.2	2.8	33	7	ABA00519	Aba00519 Human Akt
C 36	19.2	2.8	33	7	AAI47158	Aai47158 Human Akt
C 37	19.2	2.8	33	9	ADD96154	Add96154 Human Akt
C 38	19.2	2.8	33	9	ADE06642	Ade06642 Primer #4
C 39	19.2	2.8	33	9	ADE15856	Ade15856 Primer #4
C 40	19.2	2.8	33	9	ABA98210	Aba98210 Oligonuc
C 41	19.2	2.8	46	6	ABK52805	Abk52805 Human pro
C 42	19.2	2.8	50	4	AAI30792	Aai30792 Human SNP
C 43	18.8	2.8	39	2	AAI61009	Aai61009 L-galacto
C 44	18.8	2.8	40	2	AAV51259	Aav51259 Maize pol
C 45	18.8	2.8	42	4	AAI02645	Aai02645 Human CGO

ALIGNMENTS

RESULT 1  
ABA99919/c  
ID ABA99919 standard; DNA; 49 BP.  
XX  
AC ABA99919;  
XX  
DT 05-JUL-2002 (first entry)  
XX  
DE Human TNF PCR primer SEQ ID 13.  
XX  
KW Prodrug, TNF; tumour necrosis factor; selectokine; chimeric; W24; W33;  
KW cytosolic; immunomodulatory; antiangiogenic; apoptosis inducer; tenascin;  
KW gene therapy; scfv antibody O84; fibroblast activation protein; PCR;  
KW solid tumour; angiogenesis; treatment; infection; metabolic disease;  
KW primer; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200222833-Al.  
XX  
PD 21-MAR-2002.  
XX  
PF 17-SEP-2001; 2001WO-EP010730.  
XX  
PR 15-SEP-2000; 2000DE-01045592.  
XX  
PA (UYST-) UNIV STUTTGART.  
XX (PFIZ/) PFIZENMAIER K.  
XX  
PI Pfizermaier K, Wuest T, Moosmayer D, Grell M, Scheurich P;  
XX  
DR WPI; 2002-362351/39.  
XX  
PT New polypeptide prodrug, useful e.g. for treating tumors, contains  
XX targeting region, active agent and attached inhibitor that is  
XX proteolytically cleaved in target cells.  
XX  
PS Example 6; Page 47; 52pp; German.  
XX  
CC This invention describes a novel polypeptide (I) comprising, in the N to  
CC C direction, a region (R1) that recognises selectively a specific  
CC macromolecule on a cell surface and/or a component of the extracellular  
CC matrix, peptide linker, a region (R2) with biological activity for a  
CC specific target molecule, a region (R3) that has a processing site and a  
CC region (R4) that inhibits the activity of R2, by intramolecular bonding  
CC and/or interaction. The products of the invention have cytostatic,

CC immunomodulatory and antiangiogenic activity, induce apoptosis and can be  
CC used for gene therapy. Kym-1 cells (20000) were incubated with the  
CC prodrug W24, containing, essentially, the single-chain Fv antibody O54,  
CC specific for human fibroblast activation protein, trimerization linker,  
CC mutant form of the tumour necrosis factor (TNF) precursor protein, a  
CC region with a proteolytic cleavage site, and human TNF receptor-1  
CC fragment, and with trypsin (activator) for 5 minutes. After 16 hours,  
CC cell viability was determined by MTT staining. Activated W24 had LD50  
CC about 0.5 ng/ml, comparable with that for wild-type TNF and 4000 times  
CC higher than for uncleaved W24. (1), also nucleic acids encoding them and  
CC related vectors, are useful particularly for treating solid tumours  
CC and/or pathological angiogenesis, also generally for treating infections  
CC and metabolic diseases. (1) are prodrug forms of R2 that have  
CC unacceptable toxicity when administered systemically (specifically tumour  
CC necrosis factor) and allow these compounds to be administered safely with  
CC retention of, or even increase in, therapeutic activity. R2 is released  
CC only in target tissue, resulting in a high local concentration, and  
CC activity is potentiated by co-activation of receptors. This sequence  
CC represents a PCR primer for the amplification of the human TNF fragment  
CC used in the construction of the TNF-selectokine W24 and W33 prodrugs  
CC described in the disclosure of the invention  
XX  
SQ Sequence 49 BP; 12 A; 15 C; 12 G; 10 T; 0 U; 0 Other;

Query Match 3.2%; Score 21.8; DB 6; Length 49;  
Best Local Similarity 70.7%; Pred. No. 2.6e+04;  
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 74 TGGGTTCACGCTCTCCAGAGTCACGCGCGTGGCTCAG 114  
|||||  
DB 46 TGGGATCATTCGCTCTCCGGAATCGAGGTCGTGGATCCG 6

## RESULT 2

ABZ24835  
ID ABZ24835 standard; DNA; 50 BP.

AC ABZ24835;

XX 03-MAR-2003 (first entry)

DE Herpes Simplex Virus thymidine kinase PCR primer TK3'-1.

XX PCR; primer; intranuclear receptor; sex hormone receptor;  
KW androgen receptor; AR; oestrogen receptor; ER; ss.

XX Herpes Simplex Virus.

XX JP2002247986-A.

XX 03-SEP-2002.

XX 23-FEB-2001; 2001JP-00048876.

XX 23-FEB-2001; 2001JP-00048876.

XX (MITA) MITSUI CHEM INC.

XX WPI; 2003-096457/09.

XX Cells for evaluation of agonistic and antagonistic activities to a  
PT nuclear receptor of a substance, comprise a stable expression cell line  
PT of an intranuclear receptor gene and a reporter gene.

XX Example 4; Page 11; 33pp; Japanese.

XX The present invention relates to cells obtained by introduction of a  
CC reporter expression nucleic acid, which comprises a response element and  
CC a promoter downstream of the response element. The promoter controls  
CC transcription in animal host cells to significantly stimulate the  
CC expression of the reporter gene in the presence of a ligand bound to an  
CC intranuclear receptor. The cells are used for evaluation of a sex hormone  
CC receptor e.g. androgen receptor (AR) and oestrogen receptor (ER) and

CC allow sensitive and correct determination of sex hormonal activity. The  
CC present sequence is a PCR primer, which was used in an example from the  
CC invention

XX Sequence 50 BP; 7 A; 12 C; 18 G; 13 T; 0 U; 0 Other;

Query Match 3.2%; Score 21.4; DB 7; Length 50;

Best Local Similarity 66.0%; Pred. No. 3.4e+04;

Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 136 AGCACCTTCAGAAAGTTGTTGAACTTGTAGTCGGGCGCTGCATGG 182

|||||

DB 4 AGCTTCTGGGCACGCTGTTGACGCTGTTAGCGGGTCGCTGCAGGG 50

## RESULT 3

AAA71444/c  
ID AAA71444 standard; DNA; 30 BP.

XX AAA71444;

XX 01-DEC-2000 (first entry)

XX Human megasin promoter PCR primer SEQ ID NO: 11.

XX Promoter; megasin; human; protein isolation; screening. PCR primer; ss.

XX Homo sapiens.

XX WO2000043528-A1.

XX 27-JUL-2000.

XX 25-JAN-2000; 2000WO-JP000350.

XX 25-JAN-1999; 99JP-00015667.

XX (KURO/) KUROKAWA K.

XX (MIYA/) MIYATA T.

XX Miyata T;

XX WPI; 2000-543257/49.

XX DNA for promoter region of megasin useful for screening proteins.

XX Example 5; Page 38; 45pp; Japanese.

XX This invention describes a novel DNA sequence (1) representing a promoter  
CC region having part or all of a specific base sequence. The invention also  
CC describes (1) a vector containing (1); (2) a cell transformed by the  
CC above vector; and (3) protein produced using (1). (1) is useful for  
CC screening and isolating proteins (especially transcription factors).  
CC AAA71434-A71469 represent PCR primers used in the method described in the  
CC invention

XX Sequence 30 BP; 6 A; 10 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 3.1%; Score 21; DB 3; Length 30;

Best Local Similarity 82.8%; Pred. No. 3.7e+04;

Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 135 GAGCACCTTCAGAAAGTTGTTGAACTTG 163

|||||

DB 30 GAGCACCTTCAGATAGAGCTGAACCTTG 2

## RESULT 4

ABL40388/c

ID ABL40388 standard; cDNA; 33 BP.

XX ABL40388;

XX

DT 01-JUL-2002 (first entry)  
DE Primer 3 relative to HOMO phosphoryl transport protein 12.  
KW HOMO phosphoryl transport protein 12; cancer; haemopathy; phlogosis;  
KW immune disease; HIV; human immunodeficiency virus; cytostatic;  
KW haemostatic; virucide; immunomodulatory; antiinflammatory; inflammation;  
KW gene therapy; malignant tumour; PCR; primer; ss.  
OS Unidentified.  
XX  
XX WO200200698-A1.  
XX  
XX 03-JAN-2002.  
XX  
XX 14-MAY-2001; 2001WO-CN000792.  
XX  
XX 16-MAY-2000; 2000CN-00115689.  
XX  
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2002-075663/10.  
XX  
XX Polypeptide-HOMO phosphoryl transport protein 12 and encoding  
XX polynucleotide, used in diagnosis and treatment of malignant tumors,  
XX haemopathy, human immunodeficiency virus infection, immunological diseases  
XX and inflammation.  
XX  
XX Example 4; Page 18; 37pp; Chinese.  
XX  
XX The invention relates to an isolated polypeptide of polypeptide-HOMO  
XX phosphoryl transport protein 12. The activity of the polypeptide of the  
XX invention may be described as, cytostatic, haemostatic, virucide,  
XX immunomodulatory and antiinflammatory. Polypeptides and polynucleotides  
XX of the invention are used in diagnosis and treatment of malignant tumour,  
XX haemopathy, human immunodeficiency virus (HIV) infection, immunological  
XX diseases various inflammations, and phlogosis. They may also be used in  
XX gene therapy. The current sequence represents a primer relative to the  
XX HOMO phosphoryl transport protein 12 of the invention  
XX  
XX Sequence 33 BP; 5 A; 9 C; 13 G; 6 T; 0 U; 0 Other;  
Query Match 3.1%; Score 21; DB 6; Length 33;  
Best Local Similarity 82.8%; Pred. No. 3.8e+04;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 280 CACAGGCTCTCCGGCTGCGCCCTGCTAG 308  
DB 33 CACAGGCTCTCAGGGCGCCCATGCTAG 5  
RESULT 5  
AAT89030  
ID AAT89030 standard; DNA; 40 BP.  
XX  
XX AAT89030;  
XX  
XX 04-FEB-1998 (first entry)  
XX Solid phase gene HPA-2 DNA probe.  
XX  
XX Solid phase gene; synthetic gene; gene synthesis; trityl group;  
XX hydrophobic carrier; PCR primer; detection probe; HPA; ss.  
XX  
XX Synthetic.  
XX  
XX JP09257798-A.  
XX  
XX 03-OCT-1997.  
XX  
XX 19-MAR-1996; 96JP-00062885.

XX 19-MAR-1996; 96JP-00062885.  
XX (SUMQ) SUMITOMO METAL IND LTD.  
XX  
XX WPI; 1997-540228/50.  
XX  
XX Solid phase gene - useful for detection of genes in a sample.  
XX  
XX Example 1; Page 9; 12pp; Japanese.  
XX  
XX The present sequence represents a DNA probe which is used to demonstrate  
XX a new method for the detection of genes, using a synthetic gene in the  
XX solid phase. The gene has a (substituted) trityl group which binds to a  
XX hydrophobic carrier through an end protective group. The method is simple  
XX and the solid phased gene is stable. Gene amplification was carried out  
XX using a primer set to contain a point mutation determining each antigen  
XX type in the amplification region for HPA-1 to HPA-6. A synthetic DNA was  
XX prepared and a probe was immobilised on the plate. The present probe  
XX binds to HPA-2  
XX  
XX Sequence 40 BP; 7 A; 9 C; 11 G; 13 T; 0 U; 0 Other;  
Query Match 3.1%; Score 21; DB 2; Length 40;  
Best Local Similarity 73.0%; Pred. No. 4.1e+04;  
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 308 GTCTAAAGCCAGATGCCCTTCCAGGAGAGAGCTCCAGGA 344  
DB 4 GTCTCAGCTCATTTGCCCTTCAGGTAGAGCTCTTGGGA 40  
RESULT 6  
AAQ52858  
ID AAQ52858 standard; RNA; 42 BP.  
XX  
XX AAQ52858;  
XX  
XX 25-MAR-2003 (revised)  
XX 26-MAY-1994 (first entry)  
XX  
XX Cytomegalovirus target sequence 35.  
XX  
XX RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HbRNA;  
XX picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;  
XX papilloma virus; HPV; Epstein-Barr virus; EBV; TGLV;  
XX T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;  
XX influenza virus; HSV; herpes simplex virus; vector; immune response;  
XX antibody; ribozyme; viral RNA; treatment; ss.  
XX  
XX Synthetic.  
XX  
XX WO9323569-A1.  
XX  
XX 25-NOV-1993.  
XX  
XX 29-APR-1993; 93WO-US0004020.  
XX  
XX 11-MAY-1992; 92US-00882699.  
XX 14-MAY-1992; 92US-00882712.  
XX 14-MAY-1992; 92US-00882713.  
XX 14-MAY-1992; 92US-00882714.  
XX 14-MAY-1992; 92US-00882823.  
XX 14-MAY-1992; 92US-00882824.  
XX 14-MAY-1992; 92US-00882886.  
XX 14-MAY-1992; 92US-00882888.  
XX 14-MAY-1992; 92US-00882889.  
XX 14-MAY-1992; 92US-00882921.  
XX 14-MAY-1992; 92US-00882922.  
XX 14-MAY-1992; 92US-00883823.  
XX 14-MAY-1992; 92US-00883849.  
XX 14-MAY-1992; 92US-00884073.  
XX 14-MAY-1992; 92US-00884074.



```
PR 14-MAY-1992; 92US-00884333.
PR 14-MAY-1992; 92US-00884422.
PR 14-MAY-1992; 92US-00884431.
PR 14-MAY-1992; 92US-00884436.
PR 14-MAY-1992; 92US-00884521.
PR 31-JUL-1992; 92US-00923738.
PR 26-AUG-1992; 92US-00935854.
PR 18-AUG-1992; 92US-00936086.
PR 18-SEP-1992; 92US-00948359.
PR 15-OCT-1992; 92US-00963322.
PR 07-DEC-1992; 92US-00987129.
PR 07-DEC-1992; 92US-00987130.
PR 07-DEC-1992; 92US-00987133.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Draper KG, Dudycz LW, Mcswiggen JA, Macejak DG, Holecek JJ;
XX Mamone JA;
XX
XX WPI; 1993-386599/48.
XX
XX Enzymatic RNA molecules - used to inhibit viral replication, infection
XX and gene expression.
XX
XX Claim 5; Fig 13; 287pp; English.
XX
XX The sequences (AAQ52824-Q52890) are pref. Cytomegalovirus target
XX sequences for enzymatic RNA molecules. The RNA molecules are
XX complementary to a substrate binding region in the specified gene target.
XX They also have enzymatic activity, in that they specifically cleave RNA
XX in the target. The ERMs interfere with viral replication and therefore
XX have anti-viral properties. They can be used to attenuate viruses to be
XX used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated
XX on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
XX PI field.)
XX
XX Sequence 42 BP; 9 A; 9 C; 17 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 3.1%; Score 20.8; DB 2; Length 42;
XX Best Local Similarity 60.0%; Pred. No. 4.8e+04;
XX Matches 24; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
XX
XX QY 201 TTGTGGAGCAACTGTGTGCAGCGCCACCTGTCAAGAG 240
XX :||||| :|:|||||:|||||:|||||:|||||:
XX 2 UGUGGAUGACCUACGCGGCCAUCGCGGAGGAGUCAGAG 41
XX
XX RESULT 7
XX AAT80503
XX ID AAT80503 standard; DNA; 49 BP.
XX AC AAT80503;
XX
XX 31-OCT-1997 (first entry)
XX
XX Hepatoma AS-30D Type II hexokinase promoter fragment from -118.
XX
XX Response element; Z-DNA; neoplasia; hexokinase II; glycolysis; cancer;
XX gene therapy; diabetes; tumour; rat; ss.
XX
XX Rattus rattus.
XX
XX WO9704104-A2.
XX
XX 06-FEB-1997.
XX
XX 12-JUL-1996; 96WO-US011673.
XX
XX 14-JUL-1995; 95US-0001199P.
XX
XX (UYJO ) UNIV. JOHNS HOPKINS.
XX
XX Pedersen PL, Mathupala SP, Rempel A;
XX
XX
```

```
XX WPI; 1997-132643/12.
XX
XX New transcription regulating fragments of hexokinase II DNA contg.
XX response element - and methods for diagnosis or treatment of neoplasias
XX that over-express hexokinase II and for regulating glycolysis.
XX
XX Claim 1; Fig 11; 104pp; English.
XX
XX The present sequence represents a segment of the hepatoma AS-30D Type II
XX hexokinase promoter region. Response elements (transcription factor
XX binding site) in this fragment may consist of all or part of the present
XX sequence. AS-30D is a new isolated hexokinase II. The present DNA
XX fragment is capable of regulating transcription of a downstream open
XX reading frame and contains at least one response element. The present DNA
XX fragment may be coupled to a reporter gene and used to screen for
XX potential drugs that affect regulated transcription of tumour hexokinase
XX II. Alternatively it may be coupled to a toxic gene and used to treat
XX cells that over-express hexokinase II, such as those present in patients
XX with cancer. It may also be used in gene therapy to treat diabetes. The
XX DNA fragment increases glycolysis in cells and express homologous or
XX heterologous protein. Probes of the DNA fragment are used in the method
XX for diagnosing a neoplasia that over-expresses hexokinase. The new
XX response elements are active only in tumours, not in normal cells
XX
XX Sequence 49 BP; 11 A; 21 C; 12 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 3.1%; Score 20.8; DB 2; Length 49;
XX Best Local Similarity 64.8%; Pred. No. 5e+04;
XX Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
XX
XX QY 255 GCTGGGGGGCACACACACCTGTCTCCAGCAGGCTCTCCGGTGTCCCCC 302
XX :|||||:|||||:|||||:|||||:|||||:
XX 2 GCCGGAGAGGGTACACACACCTCTTCCGCGACCAATGAGCGGCCAC 49
XX
XX RESULT 8
XX AAX27583
XX ID AAX27583 standard; DNA; 35 BP.
XX AC AAX27583;
XX
XX 27-MAY-1999 (first entry)
XX
XX PPAR cDNA amplifying primer 2.
XX
XX Peroxisome proliferator-activated receptor; PPAR; reporter gene; CAT;
XX transcriptional coupling factor; screening; CBP; SRC-1; lacZ;
XX antidiabetic; antiobesity; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO9910532-A1.
XX
XX 04-MAR-1999.
XX
XX 24-AUG-1998; 98WO-JP003734.
XX
XX 27-AUG-1997; 97JP-00231084.
XX
XX (TANA ) TANABE SEIYAKU CO.
XX
XX Taniguchi T, Mizukami J;
XX
XX WPI; 1999-190635/16.
XX
XX Screening agonists/antagonists to peroxisome proliferator-activated
XX receptor - by contacting with a test cell containing a suitable reporter
XX gene.
XX
XX Example; Page 24; 34pp; Japanese.
XX
XX The invention relates to methods for identifying potential agonists or
```

RESULT 10	
AAQ22113	
ID	AAQ22113 standard; DNA; 44 BP.
XX	
XX	AAQ22113;
DT	10-JUN-1992 (first entry)
XX	
DE	S3 chimeric neurotrophic factor PCR primer 6.
XX	
XX	Polymerase chain reaction.
XX	
XX	Homo sapiens.
OS	
XX	WO9202620-A.
PN	
XX	20-FEB-1992.
PD	
XX	08-AUG-1990; 90US-00564929.
PF	
XX	08-AUG-1990; 90US-00564929.
PR	
XX	(REGS-) REGENERON PHARM INC.
XX	
PA	Shooter EM, Suter U, Ip N, Souinto SP, Furth ME, Lingsay RM;
PI	Yancopoulos GD;
PI	
XX	WPI; 1992-080074/10.
DR	
XX	
XX	New chimeric neurotrophic factors - useful in treating nervous conditions
PT	caused by trauma, surgery, ischaemia, infection, metabolic diseases,
PT	nutritional deficiency, etc.
XX	
XX	Disclosure; Page 67; 114pp; English.
PS	
XX	
CC	The sequence is that of an oligonucleotide used in the construction of
CC	chimeric neurotrophic factor S3, it represents primer 6 in the polymerase
CC	chain reaction used to produce the chimera. See also AAR21851-R21874 and
CC	AAQ22081-Q22131
XX	
XX	Sequence 44 BP; 14 A; 6 C; 17 G; 7 T; 0 U; 0 Other;
SQ	
	Query Match 3.0%; Score 20.2; DB 2; Length 44;
	Best Local Similarity 68.3%; Pred. No. 7.2e+04;
	Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY	184 AAGACTCGACAGAGCTGTGGAGCACTGTGGCCAGCGC 224
DB	4 AAGACGGCAGTGACATGCGGTAAAGGAGGTGACAGTCC 44
RESULT 11	
AAAL34545	
ID	AAAL34545 standard; DNA; 50 BP.
XX	
XX	AAAL34545;
XX	
DT	24-JAN-2002 (first entry)
XX	
XX	Human SNP oligonucleotide #7753.
XX	
XX	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW	neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW	amyloid protein; angiotensin; apolipoprotein; related protein; cadherin;
KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW	complement related protein; cytochrome; kinesin; cytokine; interferon;
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW	multifactorial disease; autoimmune disease; infection;
KW	nervous system disease; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200147944-A2.

XX PD 05-JUL-2001.  
XX PF 28-DEC-2000; 2000WO-US035498.  
XX PR 28-DEC-1999; 99US-0173419P.  
XX PR 27-DEC-2000; 2000US-00173419.  
XX PA (CURA-) CURAGEN CORP.  
XX PI Shimkets RA, Leach M;  
XX PI WPI; 2001-465210/50.  
XX DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
XX PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
XX PT autoimmune diseases and infections.  
XX PS Claim 1; Page 3631; 4143pp; English.  
XX CC The present invention relates to oligonucleotides encoding polymorphic  
XX CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
XX CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
XX CC histones, kinases, colony stimulating factors, complement related  
XX CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
XX CC protein coupled receptors and thioesterases. The present sequence is one  
XX CC such oligonucleotide, the oligonucleotides and the peptides encoded by  
XX CC them may be used in the prevention, diagnosis and treatment of diseases  
XX CC associated with inappropriate expression of the proteins listed above.  
XX CC Disorders that may be prevented, diagnosed and/or treated include  
XX CC multifactorial diseases with a genetic component, such as autoimmune  
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
XX CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
XX CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
XX CC leukaemia), diseases of the nervous system and an infection of pathogenic  
XX CC organisms.  
XX SQ Sequence 50 BP; 6 A; 18 C; 16 G; 10 T; 0 U; 0 Other;  
Query Match 3.0%; Score 20.2; DB 4; Length 50;  
Best Local Similarity 88.0%; Pred No. 7.5e+04;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 282 GCAGGCTCTCCGGTGCCTCCCTGCT 306  
Db 9 GCAGGCTCTCCGCTGCTCCCTGCT 33  
RESULT 12  
AAQ69713/c  
ID AAQ69713 standard; DNA; 50 BP.  
XX AC AAQ69713;  
XX DT 25-MAR-2003 (revised)  
XX DT 03-MAR-1995 (first entry)  
XX DE Human insulin-like growth factor II gene, target region.  
XX KW DNA protein-binding assay; test sequence; screening sequence; promoter;  
XX KW target; TATA box; Herpes Simplex Virus; HSV; origin of replication; UL9;  
XX KW transcription factor; TFIID; ds.  
XX OS Synthetic.  
XX PN WO9414980-A1.  
XX PD 07-JUL-1994.  
XX XX 20-DEC-1993; 93US-0012388.  
XX XX 23-DEC-1992; 92US-00996783.  
XX PR 17-SEP-1993; 93US-00123936.

XX PA (GENE-) GENELABS TECHNOLOGIES INC.  
XX PI Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;  
XX WPI; 1994-234711/28.  
XX DR Sequence-directed DNA-binding molecules - useful in pharmaceuticals and  
XX PT as molecular reagents.  
XX PS Claim 28; Page 443; 587pp; English.  
XX CC A DNA protein-binding assay is provided, useful for screening libraries  
XX CC of synthetic or biological cpds. for their ability to bind DNA test  
XX CC sequences. The assay is versatile in that any number of test sequences  
XX CC can be tested by placing the test sequence adjacent to a defined protein-  
XX CC binding screening sequence. Binding of mols. to these test sequences  
XX CC changes the binding characteristics of the protein mol. to its cognate  
XX CC binding sequence. When such a mol. binds the test sequence, the  
XX CC equilibrium of the DNA:protein complexes is disturbed, generating changes  
XX CC in the concentration of free DNA probe. One application of this method is  
XX CC to eucaryotic general transcription factors (e.g. TFIID), where the  
XX CC target region is typically selected from DNA sequences adjacent to the  
XX CC binding site for the eucaryotic transcription factor. Numerous exemplary  
XX CC test sequences are given: the sequences in AAQ69251-731 and AAQ69850  
XX CC correspond to promoter targets (typically, TATA box-contg. sites) for  
XX CC human genes and the sequences in AAQ69732-849 correspond to promoter  
XX CC targets for viral genes. The test sequences may also be randomly  
XX CC generated. DNA:protein interaction may be used for screening purposes,  
XX CC e.g. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see  
XX CC AAQ69851-52, AAQ69865 and AAQ69891). (Updated on 25-MAR-2003 to correct  
XX CC PN field.)  
XX SQ Sequence 50 BP; 6 A; 18 C; 21 G; 5 T; 0 U; 0 Other;  
Query Match 3.0%; Score 20; DB 2; Length 50;  
Best Local Similarity 65.9%; Pred. No. 8.6e+04;  
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
QY 259 GCGGGCACACACACCTGCTCCAGCAGGCTCTCCGGTGCCTCC 302  
Db 49 GCGGGCGCCACGCGCGGCTCTTATAGTCGCGCCAGCGCGGCC 6  
RESULT 13  
AAAT64175/c  
ID AAT64175 standard; DNA; 50 BP.  
XX AC AAT64175;  
XX DT 25-MAR-2003 (revised)  
XX DT 17-MAR-1997 (first entry)  
XX DE Human insulin-like growth factor-II gene TFIID binding site.  
XX KW Duplex DNA; target region; binding characteristic; DNA binding protein;  
XX KW TFIID; transcription factor; binding site; inhibition; enhance; cancer;  
XX KW inherited genetic disorder; ds.  
XX OS Homo sapiens.  
XX OS US5578444-A.  
XX PN 26-NOV-1996.  
XX PF 20-DEC-1993; 93US-00171389.  
XX PR 27-JUN-1991; 91US-00723618.  
XX PR 23-DEC-1992; 92US-00996783.  
XX PR 17-SEP-1993; 93US-00123936.  
XX PA (GENE-) GENELABS TECHNOLOGIES INC.  
XX XX



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DR WPI; 2002-442819/47.
PT Decreasing transcriptional activity of genes for treating infections or
PT cancer, by administration of an agent that binds to two non-overlapping
PT regions of the gene.
XX
XX Example 15; SEQ ID NO 463; 98pp; English.
XX
XX The invention relates to a method of decreasing transcriptional activity
XX in a duplex deoxyribonucleic acid (DNA) template (T1) comprising
XX contacting (T1) with a binding agent comprising at least one small duplex
XX DNA-binding molecule (T2) coupled to at least one other small duplex-
XX binding molecule that binds to a non-overlapping region of target
XX sequence (TS). The method is useful for inhibiting transcription of a
XX range of disease-related genes for treating infections (by viruses,
XX including human immunodeficiency virus, bacteria, fungi, protozoa and
XX parasites), cancer, cardiovascular, respiratory, gastrointestinal,
XX endocrine/metabolic, rheumatic/immunological, haematological,
XX neurological, psychiatric, dermatological, ophthalmological, musculo-
XX skeletal, genetic or urogenital disorders. The method provides sequence-
XX specific inhibition of transcription of pathological genes without
XX affecting transcription of cellular genes regulated by the same
XX transcription factor, and can be applied to regulation of any gene.
XX ABK32492-ABK3155 represent DNA binding molecule test sequences used in
XX the method of the invention
XX
XX Sequence 50 BP: 6 A; 18 C; 21 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 3.0%; Score 20; DB 6; Length 50;
XX Best Local Similarity 65.9%; Pred. No. 8.6e+04;
XX Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
XX
QY 259 GCGGGCACACACACCCCTCTCCACAGGCTCTCCGCTGCCCCC 302
Db 49 GCGGGCGCCACGCGCCGCTCTTATAGTCGCGCAGCCGCGGCC 6

```

Search completed: February 29, 2004, 12:01:06  
Job time : 310.274 secs



REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HAZ-015CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)526-6000  
TELEFAX: (617) 526-6000  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
FRAGMENT TYPE: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-10-361-420-37

Query Match 3.4%; Score 23; DB 14; Length 48;  
Best Local Similarity 83.9%; Pred. No. 1.1e+04;  
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 304 CACCAGCGCTGAAGCTGACACCTTCAGGGAC 334  
Db 47 CACCAGCGAGAGCCCGACCTACAGGTAC 17

RESULT 2  
US-09-736-969A-67/c  
Sequence 67, Application US/09736969A  
Patent No. US20020068302A1  
GENERAL INFORMATION:  
APPLICANT: Lu, Peter  
APPLICANT: Garman, Jonathan David  
APPLICANT: Candia III, Albert Frederick  
APPLICANT: Arbor Vita Corporation  
TITLE OF INVENTION: CLASP-4 Transmembrane Protein  
FILE REFERENCE: 020054-000411US  
CURRENT APPLICATION NUMBER: US/09/736,969A  
CURRENT FILING DATE: 2000-12-13  
PRIOR APPLICATION NUMBER: US 60/160,860  
PRIOR FILING DATE: 1999-10-21  
PRIOR APPLICATION NUMBER: US 60/162,498  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 60/170,453  
PRIOR FILING DATE: 1999-12-13  
PRIOR APPLICATION NUMBER: US 60/176,195  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: US 60/182,296  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: US 09/547,276  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: US 60/196,267  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: US 60/196,460  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: US 60/196,527  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: US 60/196,528  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: US 09/587,837  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 60/240,503  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 60/240,508  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 60/240,539  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 60/240,543  
PRIOR FILING DATE: 2000-10-13  
NUMBER OF SEQ ID NOS: 153  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 67  
LENGTH: 50  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Exon 11  
OTHER INFORMATION: ('GR2005')  
US-09-736-969A-67

Query Match 3.0%; Score 20; DB 9; Length 50;  
Best Local Similarity 72.2%; Pred. No. 7.4e+04;  
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 510 GCTCCCTGCAGCGGCTCCTGATGCAGCTGAAGC 545  
Db 44 GCTCCCGCAGCTGATGTTGCTGTCGAGCGGCATC 9

RESULT 3  
US-10-131-827-3541  
Sequence 3541, Application US/10131827  
Publication No. US20040009479A1  
GENERAL INFORMATION:  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES  
FILE REFERENCE: 506612000120  
CURRENT APPLICATION NUMBER: US/10/131,827  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: US 10/006,290  
PRIOR FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US 60/296,764  
PRIOR FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 9090  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 3541  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-131-827-3541

Query Match 3.0%; Score 20; DB 15; Length 50;  
Best Local Similarity 82.1%; Pred. No. 7.4e+04;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 439 GGCTGGCTGCGCGCATGTGCTGACTTT 466  
Db 22 GGCTGGCTCCAGAACTGTGTCCTTT 49

RESULT 4  
US-09-974-026-61/c  
Sequence 61, Application US/09974026  
Publication No. US20030194398A1  
GENERAL INFORMATION:  
APPLICANT: Tamburini, Paul P  
APPLICANT: Davis, Gary  
APPLICANT: Delaria, Katherine A  
APPLICANT: Christopher, Marlor W  
APPLICANT: Daniel, Muller K  
TITLE OF INVENTION: Human Bikunin  
FILE REFERENCE: 96-223-22  
CURRENT APPLICATION NUMBER: US/09/974,026  
CURRENT FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 09/144,428  
PRIOR FILING DATE: 1998-08-31  
PRIOR APPLICATION NUMBER: PCT/US97/03894  
PRIOR FILING DATE: 1997-03-10  
PRIOR APPLICATION NUMBER: US 08/725,251  
PRIOR FILING DATE: 1996-10-04  
PRIOR APPLICATION NUMBER: US 60/019,793  
PRIOR FILING DATE: 1996-06-14  
PRIOR APPLICATION NUMBER: US 60/013,106





```
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-753-436-67

Query Match                2.9%; Score 19.4; DB 9; Length 48;
Best Local Similarity      64.4%; Pred. No. 1.1e+05;
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 271 CACACTGCTCCAGCAGGCGCCCTCCGCTGCCCGCCACAGCCTGAA 315
      |||||||
Db 45 CAGACTGCTGCAGTTGCACCTCGGACTGGACACTGGCGCGCGCAA 1

RESULT 8
US-10-156-306-7723
; Sequence 7723, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MHE01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156.306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7723
; LENGTH: 48
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-156-306-7723

Query Match                2.9%; Score 19.4; DB 14; Length 48;
Best Local Similarity      62.1%; Pred. No. 1.1e+05;
Matches 18; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 324 CTTTCAGGAGCAGCTCCAGGAGTCTCC 352
      ||:|||||
Db 20 CCUUCAGGACAUCGUCCGGAGCUCUGC 48

RESULT 9
US-10-163-942-67/c
; Sequence 67, Application US/10163942
; Publication No. US20030199423A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemary
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/163,942
; FILING DATE: 05-Jun-2002
```

```
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/753,436
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/382,289
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/487,113
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Joseph A., Jr.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 33282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-163-942-67

Query Match                2.9%; Score 19.4; DB 14; Length 48;
Best Local Similarity      64.4%; Pred. No. 1.1e+05;
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 271 CACACTGCTCCAGCAGGCGCCCTCCGCTGCCCGCCACAGCCTGAA 315
      |||||||
Db 45 CAGACTGCTGCAGTTGCACCTCGGACTGGACACTGGCGCGCGCAA 1

RESULT 10
US-09-874-547-6
; Sequence 6, Application US/09874547
; Patent No. US20020058269A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020058269A1k, Steffen
; APPLICANT: Kassner, Paul D.
; APPLICANT: Zyomyx, Inc.
; TITLE OF INVENTION: Screening of Phage Displayed Peptides
; TITLE OF INVENTION: Without Clearing of the Cell Culture
; FILE REFERENCE: 020144-00110US
; CURRENT APPLICATION NUMBER: US/09/874,547
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/209,503
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 6
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primers for Scfv and Fab library generation (Table
; OTHER INFORMATION: I) - MHC-Backs
US-09-874-547-6
```

Query Match 2.9%; Score 19.4; DB 9; Length 50;  
Best Local Similarity 70.3%; Pred. No. 1.1e+05;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 513 CCTGTGAGCCGAGCGTCTGATGAGCTGAAGCTTTC 549  
Db 14 CCCAGCCGCCATGCGCCAGGTGCGAGCTGAAGCAGTC 50

RESULT 11  
US-10-219-195-45/c  
; Sequence 45, Application US/10219195  
; Publication No. US20030165917A1  
; GENERAL INFORMATION:  
; APPLICANT: ULLMAN, EDWIN  
; APPLICANT: WU, MING  
; APPLICANT: LIU, YEN PING  
; TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS  
; FILE REFERENCE: 3817.05-1  
; CURRENT APPLICATION NUMBER: US/10/219,195  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 60/312,505  
; PRIOR FILING DATE: 2001-08-14  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 46  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-219-195-45

Query Match 2.9%; Score 19.2; DB 14; Length 46;  
Best Local Similarity 67.5%; Pred. No. 1.2e+05;  
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 591 TCAGGAGCTCGGTACAGCGTGGCCCTGCTCTTAAAGGA 630  
Db 46 TCAAGGAGAGCTGTGCTAGTGGCCCTGGACTTCGAGCA 7

RESULT 12  
US-10-131-827-6386  
; Sequence 6386, Application US/10131827  
; Publication No. US20040009479A1  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6386  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-6386

Query Match 2.9%; Score 19.2; DB 15; Length 50;  
Best Local Similarity 87.5%; Pred. No. 1.2e+05;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 262 AGGATGCACACACTGCTCCAGCA 285  
Db 1 AGGAATGCACACACTGCTCCAGGA 24

RESULT 13  
US-10-131-827-6776/c  
; Sequence 6776, Application US/10131827  
; Publication No. US20040009479A1  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6776  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-6776

Query Match 2.9%; Score 19.2; DB 15; Length 50;  
Best Local Similarity 87.5%; Pred. No. 1.2e+05;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 262 AGGATGCACACACTGCTCCAGCA 285  
Db 50 AGGAATGCACACACTGCTCCAGGA 27

RESULT 14  
US-09-740-668A-57/c  
; Sequence 57, Application US/09740668A  
; Patent No. US20020076700A1  
; GENERAL INFORMATION:  
; APPLICANT: Shimkets, Richard  
; TITLE OF INVENTION: No. US20020076700A1el polypeptides and nucleic acids encoding sar  
; FILE REFERENCE: 15966-537 CIP  
; CURRENT APPLICATION NUMBER: US/09/740,668A  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: PCT/US99/29584  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: 09/465,512  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: 60/113,485  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 60/112,837  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 57  
; LENGTH: 36  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 2132461 PCR reverse primer  
US-09-740-668A-57

Query Match 2.8%; Score 19; DB 9; Length 36;  
Best Local Similarity 81.5%; Pred. No. 1.3e+05;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 221 AGCGCCAACTTCCCGGAGGAGCAGCTG 247

Db 36 AGCGTGACCTGCTGTGAGGAGAGCTG 10

RESULT 15

US-10-429-849-12/c  
 ; Sequence 12, Application US/10429849  
 ; Publication No. US20040029157A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TATSUKA, MASAOKI  
 ; APPLICANT: TERADA, YASUHIKO  
 ; TITLE OF INVENTION: CELL CYCLE-REGULATING PROTEINS  
 ; FILE REFERENCE: 050499/0102  
 ; CURRENT APPLICATION NUMBER: US/10/429,849  
 ; CURRENT FILING DATE: 2003-05-06  
 ; PRIOR APPLICATION NUMBER: US/09/485,534  
 ; PRIOR FILING DATE: 2000-02-14  
 ; PRIOR APPLICATION NUMBER: PCT/JP98/03641  
 ; PRIOR FILING DATE: 1998-08-17  
 ; PRIOR APPLICATION NUMBER: 235371/1997  
 ; PRIOR FILING DATE: 1997-08-15  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 12  
 ; LENGTH: 38  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer  
 US-10-429-849-12

Query Match 2.8%; Score 19; DB 12; Length 38;  
 Best Local Similarity 71.4%; Pred. No. 1.4e+05;  
 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 287 GCCTTCCTCTGCCCCCACCAGCCTGAAGCCTGA 321  
 Db 38 GCGGCGCCTCTGCTCCCTCTGCCCCCTTAGTCTGA 4

Search completed: February 29, 2004, 14:51:52  
 Job time : 271.199 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 11:48:29 ; Search time 68.0506 Seconds  
(without alignments)  
5488.301 Million cell updates/sec

Title: US-09-904-568-3\_COPY\_294\_966

Perfect score: 673

Sequence: 1 aatgtctgtgtggggctg.....gtgacgcagactcaggacg 673

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 839752

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: \*

1: /cgn2\_6/prodata/2/ina/5A-COMB.seq:\*

2: /cgn2\_6/prodata/2/ina/5B-COMB.seq:\*

3: /cgn2\_6/prodata/2/ina/6A-COMB.seq:\*

4: /cgn2\_6/prodata/2/ina/6B-COMB.seq:\*

5: /cgn2\_6/prodata/2/ina/PCUS-COMB.seq:\*

6: /cgn2\_6/prodata/2/ina/backfiles.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	23	3.4	48	3	US-08-828-533-37
C 2	23	3.4	48	4	US-09-772-153-37
C 3	19.8	2.9	45	1	US-08-176-412-5
C 4	19.8	2.9	45	2	US-08-555-268A-5
C 5	19.8	2.9	45	2	US-08-495-695B-5
C 6	19.8	2.9	45	5	PCT-US94-14436-5
C 7	19.6	2.9	45	4	US-09-144-428-61
C 8	19.6	2.9	46	2	US-08-448-418-10
C 9	19.6	2.9	46	4	US-08-146-979-10
C 10	19.4	2.9	29	3	US-08-297-395-45
C 11	19.4	2.9	48	1	US-08-482-882-67
C 12	19.4	2.9	48	1	US-08-483-389-67
C 13	19.4	2.9	48	2	US-08-487-113D-67
C 14	19.4	2.9	48	2	US-08-473-503-67
C 15	19.4	2.9	48	2	US-08-483-932-67
C 16	19.4	2.9	48	2	US-08-720-420A-67
C 17	19.4	2.9	48	3	US-08-714-017-67
C 18	19.4	2.9	48	3	US-08-475-680-67
C 19	19.4	2.9	50	4	US-09-874-547-6
C 20	19	2.8	33	1	US-08-438-639-30
C 21	19	2.8	33	1	US-07-813-338A-30
C 22	19	2.8	33	3	US-08-441-971-105
C 23	19	2.8	33	3	US-08-221-653-105
C 24	19	2.8	33	3	US-08-442-144A-105
C 25	19	2.8	33	3	US-08-441-970-105
C 26	19	2.8	45	5	PCT-US94-14106-18
C 27	18.8	2.8	36	1	US-08-624-545-16

28	18.8	2.8	38	4	US-09-474-432B-1253	Sequence 1253, Ap
29	18.8	2.8	38	4	US-09-476-387-1252	Sequence 1252, Ap
30	18.8	2.8	42	1	US-08-753-054-12	Sequence 12, Appl
31	18.6	2.8	33	4	US-09-632-575-17	Sequence 17, Appl
C 32	18.6	2.8	33	4	US-09-632-575-18	Sequence 18, Appl
33	18.6	2.8	46	4	US-09-486-241-1	Sequence 1, Appli
C 34	18.6	2.8	46	4	US-09-671-317-831	Sequence 831, App
35	18.4	2.7	45	1	US-08-176-412-6	Sequence 6, Appli
36	18.4	2.7	45	2	US-08-555-268A-6	Sequence 6, Appli
37	18.4	2.7	45	2	US-08-495-695B-6	Sequence 6, Appli
38	18.4	2.7	45	5	PCT-US94-14436-6	Sequence 6, Appli
39	18.4	2.7	47	4	US-09-671-317-538	Sequence 538, App
C 40	18.4	2.7	47	4	US-09-422-978-3508	Sequence 3508, Ap
41	18.4	2.7	50	1	US-07-972-032-75	Sequence 75, Appl
C 42	18.2	2.7	40	2	US-08-425-884-86	Sequence 86, Appl
C 43	18.2	2.7	40	2	US-08-675-502-86	Sequence 86, Appl
C 44	18.2	2.7	40	4	US-09-245-802-86	Sequence 86, Appl
C 45	18.2	2.7	41	3	US-09-171-945-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-08-828-533-37/c  
; Sequence 37, Application US/08828533  
; Patent No. 6180379  
; GENERAL INFORMATION:  
; APPLICANT: Ruderman, Joan V.  
; APPLICANT: Kirschner, Avram  
; APPLICANT: Kirschner, Marc W.  
; APPLICANT: Townsley, Fiona  
; APPLICANT: Aristarkov, Alexander  
; APPLICANT: Eytan, Esther  
; APPLICANT: Yu, Hongtao  
; TITLE OF INVENTION: NOVEL CYCLIN-SELECTIVE UBIQUITIN CARRIER  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HALE AND DORR LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: United States of America  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,533  
; FILING DATE: 31-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner Ph.D., Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HAZ-015CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 48 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; FRAGMENT TYPE: linear  
US-08-828-533-37

Query Match 3.4%; Score 23; DB 3; Length 48;  
Best Local Similarity 83.9%; Pred. No. 5.8e+03;





## RESULT 7

US-09-144-428-61/c  
; Sequence 61, Application US/09144428  
; Patent No. 6583108  
; GENERAL INFORMATION:  
; APPLICANT: BAYER CORPORATION, The  
; APPLICANT: TAMBUKUN, Paul P  
; APPLICANT: DAVIS, Gary  
; APPLICANT: DELARIA, Katherine A  
; APPLICANT: MARLOR, Christopher W  
; APPLICANT: MULLER, Daniel K  
; TITLE OF INVENTION: HUMAN BIKUNIN  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 S. Wacker Drive Suite 3200  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: USA  
; ZIP: 60606

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/144,428  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/013,106  
; FILING DATE: 11-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/019,793  
; FILING DATE: 14-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/725,251  
; FILING DATE: 04-OCT-1996

ATTORNEY/AGENT INFORMATION:  
; NAME: CHAO, Mark  
; REGISTRATION NUMBER: 37,293  
; REFERENCE/DOCKET NUMBER: 96,223-II  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 913-0001  
; TELEFAX: (312) 913-0002  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: DNA (genomic)

US-09-144-428-61  
Query Match 2.9%; Score 19.6; DB 4; Length 45;  
Best Local Similarity 73.5%; Pred. No. 3.7e+04;  
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 167 GTCAGCCTTCAGGGGAGGACTGCGGAGCG 200

DB 36 GTGCGCCATCTGCAGGGCCAGGTGAGCGGAGCG 3

## RESULT 8

US-08-448-418-10  
; Sequence 10, Application US/08448418  
; Patent No. 5837242  
; GENERAL INFORMATION:  
; APPLICANT: Holliger, Kaspar-Philipp

APPLICANT: Griffiths, Andrew D  
APPLICANT: Hoogenboom, Hendricus RJM  
APPLICANT: Malmqvist, Magnus  
APPLICANT: Marks, James D  
APPLICANT: McGuinness, Brian T  
APPLICANT: Pope, Anthony R  
APPLICANT: Prospero, Terence D  
APPLICANT: Winter, Gregory P  
TITLE OF INVENTION: Multivalent and Multispecific Binding  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall O'Toole Gerstein Murray and Borun  
STREET: 6300 Sears Tower 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,418  
FILING DATE: 14-MAY-1996  
CLASSIFICATION: C12N 15/62, 15/70, C07K 1/00  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/02492  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9225453.1  
FILING DATE: 04-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9300816.7  
FILING DATE: 16-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93303614.7  
FILING DATE: 10-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9319969.3  
FILING DATE: 22-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/32651  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA primer

US-08-448-418-10  
Query Match 2.9%; Score 19.6; DB 2; Length 46;  
Best Local Similarity 66.7%; Pred. No. 3.7e+04;  
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 510 GTCTCCTGAGCGGCTCTGATGCGAGCTGAGCTTCAG 551

DB 4 GCGGCCAGCGGCCCATGCGCCAGGTGCGAGCTGAGGAGTCAG 45

## RESULT 9

US-09-146-979-10  
; Sequence 10, Application US/09146979  
; Patent No. 6492123  
; GENERAL INFORMATION:  
; APPLICANT: Holliger, Kaspar-Philipp  
; APPLICANT: Griffiths, Andrew D  
; APPLICANT: Hoogenboom, Hendricus RJM  
; APPLICANT: Malmqvist, Magnus

APPLICANT: Marks, James D  
APPLICANT: McGuinness, Brian T  
APPLICANT: Pope, Anthony R  
APPLICANT: Prospero, Terence D  
APPLICANT: Winter, Gregory P  
TITLE OF INVENTION: Multivalent and Multispecific Binding  
TITLE OF INVENTION: Proteins, Their Manufacture and Use  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall O'Toole Gerstein Murray and Borun  
STREET: 6300 Sears Tower 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/146,979  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/448,418  
FILING DATE: 14-MAY-1996  
APPLICATION NUMBER: PCT/GB93/02492  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9225453.1  
FILING DATE: 04-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9300816.7  
FILING DATE: 16-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93303614.7  
FILING DATE: 10-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9319969.3  
FILING DATE: 22-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/32651  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA primer  
US-09-146-979-10  
Query Match 2.9%; Score 19.6; DB 4; Length 46;  
Best Local Similarity 66.7%; Pred. No. 3.7e+04;  
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 510 GTCCTGCGCCGCGCGCTGCTGAGTGCAGCTGAAGCTTTTCAG 551  
DB 4 GCGGCCAGCGCGCGCATGGCCGAGTGCAGCTGAAGGAGTCAG 45  
RESULT 10  
US-08-297-395-45/c  
Sequence 45, Application US/08297395A  
Patent No. 6039947  
GENERAL INFORMATION:  
APPLICANT: Howard L. Weiner  
APPLICANT: David A. Hafler  
TITLE OF INVENTION: EPITIDES DERIVED FROM IMMUNODOMINANT  
TITLE OF INVENTION: EPITOPES OF MYELIN BASIC PROTEIN  
FILE REFERENCE: 1010/057230S

CURRENT APPLICATION NUMBER: US/08/297,395A  
CURRENT FILING DATE: 1994-08-11  
EARLIER APPLICATION NUMBER: 08/059,189  
EARLIER FILING DATE: 1993-05-06  
EARLIER APPLICATION NUMBER: 07/502,559  
EARLIER FILING DATE: 1990-03-30  
EARLIER APPLICATION NUMBER: PCT/US88/02139  
EARLIER FILING DATE: 1988-06-24  
EARLIER APPLICATION NUMBER: 07/065,734  
EARLIER FILING DATE: 1987-06-24  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 45  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-08-297-395-45  
Query Match 2.9%; Score 19.4; DB 3; Length 29;  
Best Local Similarity 79.3%; Pred. No. 3.7e+04;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 422 GTGCCCCAGCAGCAGCGGCGCTGCTGCC 450  
DB 29 GTGTCTTACCAGCAAGGCTCTGTCTGCC 1  
RESULT 11  
US-08-482-882-67/c  
Sequence 67, Application US/08482882  
Patent No. 5773218  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Vazeux, Rosemay  
TITLE OF INVENTION: ICAM-Related Materials and Methods  
NUMBER OF SEQUENCES: 116  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,882  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,754  
FILING DATE:  
APPLICATION NUMBER: US 08/102,852  
FILING DATE: 05-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/009,266  
FILING DATE: 22-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/894,061  
FILING DATE: 05-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/889,724  
FILING DATE: 26-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,689  
FILING DATE: 27-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5773218and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32178



```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-882-67

Query Match          2.9%; Score 19.4; DB 1; Length 48;
Best Local Similarity 64.4%; Pred. No. 4.2e+04;
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 271 CACACTGCTCCAGAGCGCCCTCGCTGCCCCCACCAGCCTGAA 315
Db 45 CAGACTGCTGCAGTTGCACCTGGACTGGACACCTGGCGCGCGCAA 1

RESULT 12
US-08-483-389-67/c
Sequence 67, Application US/08483389
Patent No. 5811517
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-RELATED PROTEIN
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,389
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Suh, Young J.
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/32760
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-483-389-67

Query Match          2.9%; Score 19.4; DB 1; Length 48;
Best Local Similarity 64.4%; Pred. No. 4.2e+04;
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 271 CACACTGCTCCAGAGCGCCCTCGCTGCCCCCACCAGCCTGAA 315
Db 45 CAGACTGCTGCAGTTGCACCTGGACTGGACACCTGGCGCGCGCAA 1

RESULT 13
US-08-487-113D-67/c
Sequence 67, Application US/08487113D
Patent No. 5837822
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-8402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,113D
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5837822 and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32744
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
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US-08-487-113D-67

Query Match 2.9%; Score 19.4; DB 2; Length 48;  
Best Local Similarity 64.4%; Pred. No. 4.2e+04;  
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 271 CACACTGCTCCAGCAGCCCTCCGTCCTGCCCCCACCAGCCTGAA 315  
DB 45 CAGACTGCTGAGTTGCACCTCGGACTGGACACCTGGCGCGCAA 1

RESULT 14

US-08-473-503-67/c  
; Sequence 67, Application US/08473503  
; Patent No. 5869262  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Vazeux, Rosemay  
; TITLE OF INVENTION: ICAM-Related Materials and Methods  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/473,503  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/286,754  
; FILING DATE: 05-AUG-1994  
; APPLICATION NUMBER: US 08/102,852  
; FILING DATE: 05-AUG-1993  
; APPLICATION NUMBER: US 08/009,266  
; FILING DATE: 22-JAN-1993  
; APPLICATION NUMBER: US 07/894,061  
; FILING DATE: 05-JUN-1992  
; APPLICATION NUMBER: US 07/889,724  
; FILING DATE: 26-MAY-1992  
; APPLICATION NUMBER: US 07/827,689  
; FILING DATE: 27-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5869262and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32178  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 48 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-473-503-67

Query Match 2.9%; Score 19.4; DB 2; Length 48;  
Best Local Similarity 64.4%; Pred. No. 4.2e+04;  
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 271 CACACTGCTCCAGCAGCCCTCCGTCCTGCCCCCACCAGCCTGAA 315  
DB 45 CAGACTGCTGAGTTGCACCTCGGACTGGACACCTGGCGCGCAA 1

RESULT 15

US-08-483-932-67/c  
; Sequence 67, Application US/08483932  
; Patent No. 5880268  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Vazeux, Rosemay  
; TITLE OF INVENTION: ICAM-Related Materials and Methods  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,932  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/286,754  
; FILING DATE: 05-AUG-1994  
; APPLICATION NUMBER: US 08/102,852  
; FILING DATE: 05-AUG-1993  
; APPLICATION NUMBER: US 08/009,266  
; FILING DATE: 22-JAN-1993  
; APPLICATION NUMBER: US 07/894,061  
; FILING DATE: 05-JUN-1992  
; APPLICATION NUMBER: US 07/889,724  
; FILING DATE: 26-MAY-1992  
; APPLICATION NUMBER: US 07/827,689  
; FILING DATE: 27-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5880268and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32178  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 48 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-483-932-67

Query Match 2.9%; Score 19.4; DB 2; Length 48;  
Best Local Similarity 64.4%; Pred. No. 4.2e+04;  
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 271 CACACTGCTCCAGCAGCCCTCCGTCCTGCCCCCACCAGCCTGAA 315  
DB 45 CAGACTGCTGAGTTGCACCTCGGACTGGACACCTGGCGCGCAA 1

Mon Mar 1 10:00:10 2004

us-09-904-568-3 copy\_294\_966.szlm50.rni

Page 8

Search completed: February 29, 2004, 14:42:41  
Job time : 70.0506 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 10:34:43 ; Search time 2034.51 Seconds  
(without alignments)  
9878.168 Million cell updates/sec

Title: US-09-904-568-3\_COPY\_294\_966

Perfect score: 673

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 138346

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hcc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_nam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21.8	3.2	50	9	AU102670
C 2	20.8	3.1	50	29	AL946896
C 3	20.6	3.1	45	12	BG772081
C 4	20	3.0	46	14	H45385

5	19.8	2.9	45	14	T63738	T63738 yc23e03.r1
6	19.8	2.9	46	9	AI153463	AI153463 uc53e11.r
C 7	19.8	2.9	50	9	AU102937	AU102937 AU102937
C 8	19.8	2.9	50	9	AU103175	AU103175 AU103175
C 9	19.8	2.9	50	9	AU106019	AU106019 AU106019
C 10	19.6	2.9	50	9	AL651763	AL651763 AL651763
C 11	19.4	2.9	40	12	BI160469	BI160469 602864532
12	19.2	2.9	43	29	CG714548	CG714548 1119037B1
13	19.2	2.9	44	29	CG708599	CG708599 1119010A0
14	19.2	2.9	44	29	CG708605	CG708605 1119010A0
15	19.2	2.9	44	29	CG708611	CG708611 1119010A0
16	19.2	2.9	44	29	CG708616	CG708616 1119010A0
17	19.2	2.9	44	29	CG708624	CG708624 1119010A1
18	19.2	2.9	44	29	CG708627	CG708627 1119010A1
19	19.2	2.9	44	29	CG708670	CG708670 1119010C0
20	19.2	2.9	44	29	CG708679	CG708679 1119010C0
21	19.2	2.9	44	29	CG708685	CG708685 1119010C0
22	19.2	2.9	44	29	CG708716	CG708716 1119010D0
23	19.2	2.9	44	29	CG708728	CG708728 1119010D1
24	19.2	2.9	44	29	CG708745	CG708745 1119010E0
25	19.2	2.9	44	29	CG708750	CG708750 1119010E0
26	19.2	2.9	44	29	CG708753	CG708753 1119010E1
27	19.2	2.9	44	29	CG708770	CG708770 1119010F0
28	19.2	2.9	44	29	CG708785	CG708785 1119010F0
29	19.2	2.9	44	29	CG708791	CG708791 1119010F1
30	19.2	2.9	44	29	CG708817	CG708817 1119010G0
31	19.2	2.9	44	29	CG708833	CG708833 1119010H0
32	19.2	2.9	44	29	CG708836	CG708836 1119010H0
33	19.2	2.9	44	29	CG708839	CG708839 1119010H0
34	19.2	2.9	44	29	CG708859	CG708859 1119010H1
35	19.2	2.9	44	29	CG708865	CG708865 1119011A0
36	19.2	2.9	44	29	CG708904	CG708904 1119011B0
37	19.2	2.9	44	29	CG708937	CG708937 1119011C0
38	19.2	2.9	44	29	CG708940	CG708940 1119011C0
39	19.2	2.9	44	29	CG708943	CG708943 1119011C0
40	19.2	2.9	44	29	CG708980	CG708980 1119011D0
41	19.2	2.9	44	29	CG708989	CG708989 1119011D1
42	19.2	2.9	44	29	CG708999	CG708999 1119011E0
43	19.2	2.9	44	29	CG709002	CG709002 1119011E0
44	19.2	2.9	44	29	CG709025	CG709025 1119011E1
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ALIGNMENTS

RESULT 1  
AU102670/c  
LOCUS AU102670 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION AU102670 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
CAS07213, mRNA sequence.  
ACCESSION AU102670  
VERSION AU102670.1 GI:13552191  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
Kata, H., Oka, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
TITLE Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
MEDLINE 21270072  
PUBMED 11375929  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and



```

DEFINITION YN99cl2.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone
IMAGE:176566 5', similar to SP:TF52_MOUSE P10712 TRANSCRIPTION
FACTOR S-II ;, mRNA sequence.
H45385
H45385.1 GI:921437
EST.
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: M13RPI
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="GDB:3838762"
/db_xref="taxon:9606"
/clone="IMAGE:176566"
/sex="Male"
/dev_stage="55-Year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b5HB55Y"
/notes="Organ: brain; Vector: p7T3D (Pharmacia) with a
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strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAGTGGGAGCGCGCGCTTTTGTGTTTGTGTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 53. Library constructed by Bento
Soares and M.Fatima Bonaldo. The adult brain RNA was
provided by Dr. Donald H. Gilden. Tissue was acquired
17-18 hours after death which occurred in consequence of a
ruptured aortic aneurysm. RNA was prepared from a pool of
tissues representing the following areas of the brain:
frontal, parietal, temporal and occipital cortex from the
left and right hemispheres, subcortical white matter,
basal ganglia, thalamus, cerebellum, midbrain, pons and
medulla."

FEATURES
source
1..46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3838762"
/db_xref="taxon:9606"
/clone="IMAGE:176566"
/sex="Male"
/dev_stage="55-Year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b5HB55Y"
/notes="Organ: brain; Vector: p7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAGTGGGAGCGCGCGCTTTTGTGTTTGTGTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 53. Library constructed by Bento
Soares and M.Fatima Bonaldo. The adult brain RNA was
provided by Dr. Donald H. Gilden. Tissue was acquired
17-18 hours after death which occurred in consequence of a
ruptured aortic aneurysm. RNA was prepared from a pool of
tissues representing the following areas of the brain:
frontal, parietal, temporal and occipital cortex from the
left and right hemispheres, subcortical white matter,
basal ganglia, thalamus, cerebellum, midbrain, pons and
medulla."

ORIGIN
Query Match 3.0%; Score 20; DB 14; Length 46;
Best Local Similarity 72.2%; Pred. No. 2.3e+06;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 351 GCATCCCCAAGACCTGCTGGGACTTCGCCAGCG 386
DB 41 GCTTCTCCAGACTTGATGAGAGACTTGGCCAGTG 6

RESULT 5
LOCUS T63738
DEFINITION YC23e03.r1 Stragatene lung (#937210) Homo sapiens cDNA clone
IMAGE:81532 5', similar to gb:X55715 40S RIBOSOMAL PROTEIN S3
(HUMAN);, mRNA sequence.
T63738
T63738.1 GI:667603
EST.
T63738.1 Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 45)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevasakis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
8889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 55
High quality sequence stops: 37
Source: IMAGE Consortium, LLNL This
clone is available royalty-free through LLNL; contact the IMAGE
Consortium (info@image.llnl.gov) for further information.
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Seq primer: M13RPI
High quality sequence stop: 37.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:81532"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stragatene lung (#937210)"
/notes="Organ: lung; Vector: pBluescript SK-; Site 1:
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Oligo dt. normal lung. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Query Match 2.9%; Score 19.8; DB 14; Length 45;
Best Local Similarity 77.4%; Pred. No. 2.5e+06;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 628 GGAGATGCGAGATCTCGAGAAGAGGTGTGTGAG 658
DB 1 GAAGATGCGTACTCTGGAGTTGAGTGGCAG 31

RESULT 6
LOCUS A1153463
DEFINITION uc53e11.r1 Soares thymus 2NDMT Mus musculus cDNA clone
IMAGE:1429388 5', similar to SW:PHLX_RABIT Q05017 PHOSPHOLIPASE
ADRB-B PRECURSOR ;, mRNA sequence.
A1153463
A1153463.1 GI:3681932

```

```
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE The WashU-HMMI Mouse EST Project
JOURNAL
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:913456
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..46
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1429388"
/sex="male"
/tissue_type="Thymus"
/dev_stages="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares thymus 2NbMT"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATGAGTCGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
ORIGIN
Query Match 2.9%; Score 19.8; DB 9; Length 46;
Best Local Similarity 69.2%; Pred. No. 2.6e+06;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
FEATURES
source
1..175
CCTGCAGGGGAGGACTGCGGAGACGCGTGTGCGAGCTCT 213
|||||
4 CATGGAGCGTGAGGACTTCGCACTCCTGTCGAGCGCTT 42
|||||
RESULT 7
AUI02937/c
LOCUS
DEFINITION AUI02937 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
LNG10694, mRNA sequence.
ACCESSION AUI02937.1 GI:13552458
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Fukuyota, K., Tanaka, T., Morishita, S., Okubo, K.,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S., Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG10694"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match 2.9%; Score 19.8; DB 9; Length 50;
Best Local Similarity 69.2%; Pred. No. 2.7e+06;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
FEATURES
source
1..564
ACGCGTTTGAAGTCCCAAGCCAGCAAGTTCAGGAGCTGC 602
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40 ACGGCGTGAGCGTACCCGAGCGCATGTCCTCCAGGAGCTAC 2
|||||
RESULT 8
AUI03175/c
LOCUS
DEFINITION AUI03175 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSI07628, mRNA sequence.
ACCESSION AUI03175.1 GI:13552696
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Fukuyota, K., Tanaka, T., Morishita, S., Okubo, K.,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S., Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HSI07628"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S., Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HSI07628"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
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/clone="IMAGE:5018743"  
/tissue\_type="epithelioid carcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_42"  
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected 500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 2.9%; Score 19.4; DB 12; Length 40;  
Best Local Similarity 70.3%; Pred. No. 2.9e+06;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 346 GCTCTGCTATCCCAAGACCTGCTGGGACTTGGCC 382

Db 37 GCTCGGACCCCGGACCCGCTCGGGATCTCGCC 1

## RESULT 12

CG714548  
LOCUS 1119037B11.1EL\_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic  
DEFINITION survey sequence.  
CG714548  
ACCESSION CG714548.1 GI:37741009

VERSION GSS.

KEYWORDS

SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 43)

Walbot.V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

JOURNAL

COMMENT

Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1119037 row: 32

Class: transposon-tagged.

Location/Qualifiers

1..43

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="1119 - RescueMu Grid AA"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'www.zmdb.iastate.edu' and follow the links for

'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA

was extracted from leaf strips, double digested using

BamHI and BglII, and ligated to form circular plasmids.

DH10B cells were transformed and then screened on LB

Plates with ampicillin."

## ORIGIN

Query Match 2.9%; Score 19.2; DB 29; Length 43;  
Best Local Similarity 67.5%; Pred. No. 3.3e+06;  
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 229 CTTGCCGAGGAGCAGCTGGTGGCTGCTGGCAGCATG 268

Db 1 CTTGCCGAGGAGCAGCAGCATCTATCTCTGAGCGACAGG 40

## RESULT 13

CG708599

LOCUS

DEFINITION

CG708599

ACCESSION

CG708599.1

KEYWORDS

SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 44)

Walbot.V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

JOURNAL

COMMENT

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1119010 row: 33

Class: transposon-tagged.

Location/Qualifiers

1..44

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="1119 - RescueMu Grid AA"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'www.zmdb.iastate.edu' and follow the links for

'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA

was extracted from leaf strips, double digested using

BamHI and BglII, and ligated to form circular plasmids.

DH10B cells were transformed and then screened on LB

plates with ampicillin."

Query, Match 2.9%; Score 19.2; DB 29; Length 44;

Best Local Similarity 67.5%; Pred. No. 3.3e+06;

Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 229 CTTGCCGAGGAGCAGCTGGTGGCTGCTGGCAGCATG 268

Db 2 CTTGCCGAGGAGCAGCAGCATCTATCTCTGAGCGACAGG 41

## RESULT 14

CG708605  
LOCUS  
DEFINITION  
CG708605 44 bp DNA linear GSS 20-OCT-2003  
1119010A04.1EL.x1 1119 - RescueMu Grid AA Zea mays genomic, genomic  
survey sequence.

ACCESSION  
CG708605  
VERSION  
CG708605.1 GI:37734511  
KEYWORDS  
GSS.

## SOURCE

Zea mays

## ORGANISM

Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

1 (bases 1 to 44)  
Walbot,V.  
Maize genomic sequences found using engineered RescueMu transposon  
Unpublished (2001)

## JOURNAL

## COMMENT

Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227

Fax: 650 725 8221  
Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.

Plate: 1119010 row: 33

Class: transposon-tagged.

## FEATURES

source

1..44

Location/Qualifiers

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="1119 - RescueMu Grid AA"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'www.zmdb.iastate.edu' and follow the links for

'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA

was extracted from leaf strips, double digested using

BamHI and BglII, and ligated to form circular plasmids.

DH10B cells were transformed and then screened on LB

plates with ampicillin."

## ORIGIN

Query Match 2.9%; Score 19.2; DB 29; Length 44;

Best Local Similarity 67.5%; Pred. No. 3.3e+06;

Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY

229 CCTGCCGAGGAGCAGCTGGTGCCCTGCTGGCAGGCATG 268

||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 2 CCTGCCGAGGAGCAGCAGCATCTCATCTCTGAGCGACAGG 41

## RESULT 15

CG708611  
LOCUS  
DEFINITION  
CG708611 44 bp DNA linear GSS 20-OCT-2003  
1119010A06.1EL.x1 1119 - RescueMu Grid AA Zea mays genomic, genomic  
survey sequence.

ACCESSION  
CG708611  
VERSION  
CG708611.1 GI:37734517  
KEYWORDS  
GSS.

## SOURCE

Zea mays

## ORGANISM

Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1119010 row: 33

Class: transposon-tagged.

## FEATURES

source

1..44

Location/Qualifiers

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="1119 - RescueMu Grid AA"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'www.zmdb.iastate.edu' and follow the links for

'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA

was extracted from leaf strips, double digested using

BamHI and BglII, and ligated to form circular plasmids.

DH10B cells were transformed and then screened on LB

plates with ampicillin."

## ORIGIN

Query Match 2.9%; Score 19.2; DB 29; Length 44;

Best Local Similarity 67.5%; Pred. No. 3.3e+06;

Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY

229 CCTGCCGAGGAGCAGCTGGTGCCCTGCTGGCAGGCATG 268

||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 2 CCTGCCGAGGAGCAGCAGCATCTCATCTCTGAGCGACAGG 41

Search completed: February 29, 2004, 14:40:15

Job time : 2037.51 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 10:05:33 ; Search time 2729.03 Seconds  
(without alignments)  
10688.739 Million cell updates/sec

Title: US-09-904-568-3\_COPY\_294\_966

Perfect score: 673

Sequence: 1 aatgtctgctgtggtgggctg.....gtgagcgagactgcaggac 673

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1603530

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*\*

1: gb\_ba:\*\*

2: gb\_htg:\*\*

3: gb\_in:\*\*

4: gb\_on:\*\*

5: gb\_ov:\*\*

6: gb\_pat:\*\*

7: gb\_ph:\*\*

8: gb\_pl:\*\*

9: gb\_pr:\*\*

10: gb\_ro:\*\*

11: gb\_sts:\*\*

12: gb\_sy:\*\*

13: gb\_un:\*\*

14: gb\_vi:\*\*

15: em\_ba:\*\*

16: em\_fun:\*\*

17: em\_hum:\*\*

18: em\_in:\*\*

19: em\_mu:\*\*

20: em\_mu:\*\*

21: em\_or:\*\*

22: em\_ov:\*\*

23: em\_pat:\*\*

24: em\_ph:\*\*

25: em\_pl:\*\*

26: em\_ro:\*\*

27: em\_sts:\*\*

28: em\_un:\*\*

29: em\_vi:\*\*

30: em\_htg\_hum:\*\*

31: em\_htg\_inv:\*\*

32: em\_htg\_other:\*\*

33: em\_htg\_mus:\*\*

34: em\_htg\_pin:\*\*

35: em\_htg\_rod:\*\*

36: em\_htg\_man:\*\*

37: em\_htg\_vrt:\*\*

38: em\_sy:\*\*

39: em\_htgo\_hum:\*\*

40: em\_htgo\_mus:\*\*

41: em\_htgo\_other:\*\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	23	3.4	48	6	AR127012	AR127012 Sequence
C 2	23	3.4	48	6	AR285578	AR285578 Sequence
C 3	21	3.1	45	6	A76101	A76101 Sequence 40
C 4	20.6	3.1	40	6	AX517113	AX517113 Sequence
C 5	20.6	3.1	40	6	AX519642	AX519642 Sequence
C 6	20.2	3.0	42	6	E41550	E41550 Method for
C 7	20.2	3.0	42	6	BD013091	BD013091 Method for
C 8	20	3.0	50	5	CHKGDCG	D90240 Gallus gall
C 9	20	3.0	50	6	AX173088	AX173088 Sequence
C 10	19.8	2.9	45	6	AR075912	AR075912 Sequence
C 11	19.8	2.9	45	6	AR083198	AR083198 Sequence
C 12	19.8	2.9	45	6	BD247107	BD247107 Improved
C 13	19.8	2.9	45	6	I20781	I20781 Sequence 5
C 14	19.8	2.9	48	6	BD237452	BD237452 Single nu
C 15	19.8	2.9	48	6	BD270516	BD270516 Method, 7
C 16	19.8	2.9	48	6	AX026686	AX026686 Sequence
C 17	19.8	2.9	50	9	AF057510	AF057510 Homo sapi
C 18	19.6	2.9	41	6	AX513948	AX513948 Sequence
C 19	19.6	2.9	41	6	AX519287	AX519287 Sequence
C 20	19.6	2.9	45	6	BD247648	BD247648 A method
C 21	19.6	2.9	45	6	AR345117	AR345117 Sequence
C 22	19.6	2.9	46	6	A38923	A38923 Sequence 10
C 23	19.6	2.9	46	6	AR054319	AR054319 Sequence
C 24	19.6	2.9	46	6	AR265069	AR265069 Sequence
C 25	19.6	2.9	48	6	AX221581	AX221581 Sequence
C 26	19.4	2.9	31	6	E26067	E26067 Oligonucleo
C 27	19.4	2.9	48	6	AR013871	AR013871 Sequence
C 28	19.4	2.9	48	6	AR033825	AR033825 Sequence
C 29	19.4	2.9	48	6	AR042485	AR042485 Sequence
C 30	19.4	2.9	48	6	AR058365	AR058365 Sequence
C 31	19.4	2.9	48	6	AR088191	AR088191 Sequence
C 32	19.4	2.9	48	6	BD237453	BD237453 Single nu
C 33	19.4	2.9	48	6	BD270517	BD270517 Method, 7
C 34	19.4	2.9	48	6	AX026687	AX026687 Sequence
C 35	19.4	2.9	48	6	AX583009	AX583009 Sequence
C 36	19.4	2.9	50	6	AX157594	AX157594 Sequence
C 37	19.4	2.9	50	6	AX351171	AX351171 Sequence
C 38	19.2	2.9	41	6	AX516097	AX516097 Sequence
C 39	19.2	2.9	41	6	AX517503	AX517503 Sequence
C 40	19.2	2.9	45	6	AX840266	AX840266 Sequence
C 41	19	2.8	33	6	AR004376	AR004376 Sequence
C 42	19	2.8	33	6	AR097167	AR097167 Sequence
C 43	19	2.8	33	6	AR130665	AR130665 Sequence
C 44	19	2.8	33	6	AR172014	AR172014 Sequence
C 45	19	2.8	33	6	I82851	I82851 Sequence 30

ALIGNMENTS

RESULT 1  
AR127012/c  
LOCUS AR127012 48 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 37 from patent US 6180379.  
ACCESSION AR127012  
VERSION AR127012.1 GI:14113605  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Ruderman,J.V., Hershko,A., Kirschner,M.W., Townsley,F.,  
Aristarkov,A., Eytan,E. and Yu,H.  
TITLE Cyclin-selective ubiquitin carrier polypeptides  
JOURNAL Patent: US 6180379-A 37 30-JAN-2001;

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FEATURES
  source
    Location/Qualifiers
    1..48
    /organism="unknown"
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ORIGIN
  Query Match      3.4%; Score 23; DB 6; Length 48;
  Best Local Similarity 83.9%; Pred. No. 2.5e+06;
  Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 304 CACCAGCCTGAGCCTGACACCTTCAGGGAC 334
Db 47 CACCAGCCAGGAGCCCGACACCTACAGGTAC 17
RESULT 2
LOCUS AR285578/c
DEFINITION Sequence 37 from patent US 6528633.
ACCESSION AR285578
VERSION AR285578.1 GI:29723140
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 48)
  Ruderman,J.V., Herskho,A., Kirschner,M.W., Townsley,F.,
  Aristarkov,A., Eytan,E. and Yu.H.
  Cyclic-selective ubiquitin carrier polypeptides
  Patent: US 6528633-A 37 04-MAR-2003;
  Location/Qualifiers
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  /organism="unknown"
  /mol_type="unassigned DNA"
ORIGIN
  Query Match      3.4%; Score 23; DB 6; Length 48;
  Best Local Similarity 83.9%; Pred. No. 2.5e+06;
  Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 304 CACCAGCCTGAGCCTGACACCTTCAGGGAC 334
Db 47 CACCAGCCAGGAGCCCGACACCTACAGGTAC 17
RESULT 3
LOCUS A76101/c
DEFINITION Sequence 40 from Patent WO9320210.
ACCESSION A76101
VERSION A76101.1 GI:6088242
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
  1 (bases 1 to 45)
  Taylor,G. and Stott,E.J.
  ANTIBODIES FOR TREATMENT AND PREVENTION OF RESPIRATORY SYNCYTIAL
  VIRUS INFECTION
  Patent: WO 9320210-A 40 14-OCT-1993;
  JOURNAL SCOTGEN LTD (GB); TAYLOR GERALDINE (GB)
  Location/Qualifiers
  1..45
  /organism="unidentified"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32644"
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  Query Match      3.1%; Score 21; DB 6; Length 45;
  Best Local Similarity 66.7%; Pred. No. 6.2e+06;
  Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 42 CTGGTGATAGTACAGAGTGGCCGAGTGAGTTCCTTGGGGGCCCCAGC 86
Db 45 CTGCTGATCTACAGAGTTCCTCAACCGATTTCTGTGTGCCAAGC 1
RESULT 4
LOCUS AX517113/c
DEFINITION Sequence 3311 from Patent WO02052044.
ACCESSION AX517113
VERSION AX517113.1 GI:23565449
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1
  Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
  Detection of genetic polymorphisms
  Patent: WO 02052044-A 3311 04-JUL-2002;
  Riken (JP)
  Location/Qualifiers
  1..40
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"
ORIGIN
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  Best Local Similarity 74.3%; Pred. No. 7.6e+06;
  Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 133 CAGGAGCAGCTTCAGAAAGTGTCTGAAGTTTGTGG 167
Db 36 CAGCAGCAAGCTGGGAGAGTAGCTGCAGATTGTGG 2
RESULT 5
LOCUS AX519642/c
DEFINITION Sequence 5840 from Patent WO02052044.
ACCESSION AX519642
VERSION AX519642.1 GI:23569993
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1
  Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
  Detection of genetic polymorphisms
  Patent: WO 02052044-A 5840 04-JUL-2002;
  Riken (JP)
  Location/Qualifiers
  1..40
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"
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  Query Match      3.1%; Score 20.6; DB 6; Length 40;
  Best Local Similarity 74.3%; Pred. No. 7.6e+06;
  Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 133 CAGGAGCAGCTTCAGAAAGTGTCTGAAGTTTGTGG 167
Db 36 CAGCAGCAAGCTGGGAGAGTAGCTGCAGATTGTGG 2
RESULT 6
LOCUS E41550/c
DEFINITION Method for yielding male abortive plants.
ACCESSION E41550
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VERSION      BA1550.1 GI:22553203
KEYWORDS     JP 2001095406-A/2.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 42)
AUTHORS      Hamada, K. and Nakakido, F.
TITLE        Method for yielding male abortive plants
JOURNAL      Patent: JP 2001095406-A 2 10-APR-2001;
              JAPAN TOBACCO INC
COMMENT      OS Artificial Sequence
              PN JP 2001095406-A/2
              PF 30-SEP-1999 JP 1999279307
              PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
              PC A01H5/00, C12N5/10, C12N15/09, C12N5/00, C12N15/00 CC
              172del-R
FH Key       Location/Qualifiers.
FEATURES     source
              1..42
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
ORIGIN
Query Match      3.0%; Score 20.2; DB 6; Length 42;
Best Local Similarity 68.3%; Pred. No. 9e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 482 GTAGCAATCTCCACCACTGCCCTGGCTCGCTCCCTGCAGCC 522
Db 42 GTAAATTTGCCCCCATGTGCTGGCTGGCTGACTGCAGCC 2

RESULT 7
BD013091/c
LOCUS        BD013091
DEFINITION   Method for producing male-sterile plant.
ACCESSION    BD013091
VERSION      BD013091.1 GI:22093280
KEYWORDS     WO 0124616-A/2.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 42)
AUTHORS      Hamada, K. and Nakakido, F.
TITLE        Method for producing male-sterile plant
JOURNAL      Patent: WO 0124616-A 2 12-APR-2001;
              JAPAN TOBACCO INC, KAZUYUKI HAMADA, FUMIO NAKAKIDO
COMMENT      OS Artificial Sequence
              PN WO 0124616-A/2
              PD 12-APR-2001
              PF 12-SEP-2000 WO 2000JP006222
              PR 30-SEP-1999 JP 99P 279307
              PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
              PC A01H5/00, C12N15/11, C12N15/63, C12N15/82
              CC Primer 172del-R
FH Key       Location/Qualifiers.
FEATURES     source
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              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
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Query Match      3.0%; Score 20.2; DB 6; Length 42;
Best Local Similarity 68.3%; Pred. No. 9e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 482 GTAGCAATCTCCACCACTGCCCTGGCTCGCTCCCTGCAGCC 522
Db 42 GTAAATTTGCCCCCATGTGCTGGCTGGCTGACTGCAGCC 2

us-09-904-568-3_copy_294_966.szlm50.rge

RESULT 8
CHKGDCG
LOCUS        Gallus gallus gene for glycine decarboxylase, partial cds.
DEFINITION   D90240
ACCESSION    D90240
VERSION      D90240.1 GI:222818
KEYWORDS     Gallus gallus (chicken)
SOURCE       Gallus gallus
ORGANISM     Gallus gallus
REFERENCE    1 (bases 1 to 50)
AUTHORS      Kume, A., Koyata, H., Sakakibara, T., Ishiguro, Y., Kure, S. and
              Hiraga, K.
TITLE        The glycine cleavage system. Molecular cloning of the chicken and
              human glycine decarboxylase cDNAs and some characteristics involved
              in the deduced protein structures
JOURNAL      J. Biol. Chem. 266 (5), 3323-3329 (1991)
MEDLINE      91131643
PUBMED       1993704
COMMENT      These data kindly submitted in computer readable form by: Koichi
              Hiraga
              Department of Biochemistry
              Toyama Medical and Pharmaceutical University
              School of Medicine
              2630 Sugitani, Toyama
              Toyama 930-01
              Japan
              Phone: 81-764-34-2281 x2330
              Fax: 81-764-34-4656.
              Location/Qualifiers
              1..50
              /organism="Gallus gallus"
              /mol_type="genomic DNA"
              /db_xref="taxon:9031"
              /note="clones pCP15b, 23a, 110b, and 112a]"
              11..>50
              /note="pyridoxal phosphate enzyme"
              /codon_start=1
              /product="glycine decarboxylase"
              /protein_id="BAH4287.1"
              /db_xref="GI:222819"
              /translation="MQSGRWGRLAA"

ORIGIN
Query Match      3.0%; Score 20; DB 5; Length 50;
Best Local Similarity 65.9%; Pred. No. 9.5e+06;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 316 GCCTGACACCTTCAGGGACCACTCCAGGAGCTCTGCTATCCCC 359
Db 49 GGCGCCAGCGCGCCGCCACCAAGCGCGCGCTCTGCTATGACCC 6

RESULT 9
AX173088/c
LOCUS        AX173088
DEFINITION   Sequence 67 from Patent WO0142294.
ACCESSION    AX173088
VERSION      AX173088.1 GI:14597988
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1
AUTHORS      Lu, P., Garman, J. D. and Candia, A. F.
TITLE        Clasp-4 transmembrane protein
JOURNAL      Patent: WO 0142294-A 67 14-JUN-2001;
              Arbor Vita Corporation (US)
              Location/Qualifiers
              1..50
              /db_xref="taxon:9031"
              /note="clones pCP15b, 23a, 110b, and 112a]"
              11..>50
              /note="pyridoxal phosphate enzyme"
              /codon_start=1
              /product="glycine decarboxylase"
              /protein_id="BAH4287.1"
              /db_xref="GI:222819"
              /translation="MQSGRWGRLAA"

ORIGIN
Query Match      3.0%; Score 20.2; DB 6; Length 42;
Best Local Similarity 68.3%; Pred. No. 9e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 482 GTAGCAATCTCCACCACTGCCCTGGCTCGCTCCCTGCAGCC 522
Db 42 GTAAATTTGCCCCCATGTGCTGGCTGGCTGACTGCAGCC 2
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2



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Sequence:

1 atgtctgcttgggggctgc.....gtgagcgcaactgcaggac 672

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Gapop 10.0 , Gapext 1.0

Searched: 2353733 seqs, 1803733377 residues

Total number of hits satisfying chosen parameters: 1385142

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

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- 2: /cgn2\_6/prodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
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- 4: /cgn2\_6/prodata/2/pubpna/US06\_PUBCOMB.seq.\*
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- 6: /cgn2\_6/prodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq.\*
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- 9: /cgn2\_6/prodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/prodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/prodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/prodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/prodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq.\*

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#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.2	3.0	35	13	US-10-109-886-2
2	20	3.0	50	10	Sequence 2, Appli
3	20	3.0	50	15	Sequence 463, App
4	19.8	2.9	42	15	Sequence 677, App
5	19.6	2.9	50	14	Sequence 56, Appli
6	19.4	2.9	50	14	Sequence 8, Appli
7	19.2	2.9	44	15	Sequence 309, App
8	19.2	2.9	44	14	Sequence 19, Appli
9	19.2	2.9	47	15	Sequence 19, Appli
10	19.2	2.9	50	15	Sequence 2676, Ap
11	19.2	2.9	50	15	Sequence 1287, Ap
12	18.8	2.8	50	10	Sequence 1362, Ap
13	18.6	2.8	38	15	Sequence 23, Appli
14	18.6	2.8	38	15	Sequence 31, Appli
15	18.6	2.8	43	14	Sequence 15, Appli

C	16	18.6	2.8	50	15	US-10-131-827-5574	Sequence 5574, App
	17	18.4	2.7	37	9	US-09-996-606-5	Sequence 5, Appli
	18	18.4	2.7	40	15	US-10-447-839A-78	Sequence 78, Appli
	19	18.4	2.7	50	9	US-09-989-722-251	Sequence 251, App
	20	18.4	2.7	50	9	US-09-989-723-251	Sequence 251, App
	21	18.4	2.7	50	9	US-09-989-273-251	Sequence 251, App
	22	18.4	2.7	50	9	US-09-989-721-251	Sequence 251, App
	23	18.4	2.7	50	9	US-09-989-731-251	Sequence 251, App
	24	18.4	2.7	50	9	US-09-989-732-251	Sequence 251, App
	25	18.4	2.7	50	9	US-09-991-073-251	Sequence 251, App
	26	18.4	2.7	50	9	US-09-990-442-251	Sequence 251, App
	27	18.4	2.7	50	9	US-09-991-163-251	Sequence 251, App
	28	18.4	2.7	50	9	US-09-993-604-251	Sequence 251, App
	29	18.4	2.7	50	9	US-09-990-456-251	Sequence 251, App
	30	18.4	2.7	50	9	US-09-989-721-251	Sequence 251, App
	31	18.4	2.7	50	9	US-09-992-598-251	Sequence 251, App
	32	18.4	2.7	50	9	US-09-989-298A-251	Sequence 251, App
	33	18.4	2.7	50	9	US-09-989-735-251	Sequence 251, App
	34	18.4	2.7	50	9	US-09-990-444-251	Sequence 251, App
	35	18.4	2.7	50	9	US-09-991-181-251	Sequence 251, App
	36	18.4	2.7	50	9	US-09-989-730-251	Sequence 251, App
	37	18.4	2.7	50	9	US-09-990-436-251	Sequence 251, App
	38	18.4	2.7	50	9	US-09-993-687-251	Sequence 251, App
	39	18.4	2.7	50	10	US-09-989-734-251	Sequence 251, App
	40	18.4	2.7	50	10	US-09-997-653-251	Sequence 251, App
	41	18.4	2.7	50	10	US-09-993-667-251	Sequence 251, App
	42	18.4	2.7	50	10	US-09-997-428-251	Sequence 251, App
	43	18.4	2.7	50	10	US-09-997-666-251	Sequence 251, App
	44	18.4	2.7	50	10	US-09-990-438-251	Sequence 251, App
	45	18.4	2.7	50	10	US-09-990-562-251	Sequence 251, App

#### ALIGNMENTS

#### RESULT 1

US-10-109-886-2  
; Sequence 2, Application US/10109886  
; Publication No. US20020119499A1  
; GENERAL INFORMATION:  
; APPLICANT: TANABE SEIVAKU CO. LTD.  
; APPLICANT: TANIGUCHI, Tomoyasu  
; APPLICANT: MIZUKAMI, Junko  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND  
; FILE REFERENCE: TANIGUCHI=6  
; CURRENT APPLICATION NUMBER: US/10109,886  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 09/514,247  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: PCT/JF98/03734  
; PRIOR FILING DATE: 1998-08-24  
; PRIOR APPLICATION NUMBER: JP231084/1997  
; PRIOR FILING DATE: 1997-08-27  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially synthesized primer sequence  
US-10-109-886-2

Query Match 3.0%; Score 20.2; DB 13; Length 35;  
Best Local Similarity 75.8%; Pred. No. 2e+04;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 86 CCTCTCAGAAAGTACGGCGCTCAGCTCT 118

Db 1 CCGCTCAGAAATGTGGCAGTGGCTCAGGACT 33



## RESULT 2

US-09-993-346-463/c  
; Sequence 463, Application US/09993346  
; Publication No. US20030124530A1  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Cynthia A.  
; Cantor, Charles R.  
; Andrews, Beth M.  
; Turin, Lisa M.  
; Fry, Kirk E.

TITLE OF INVENTION: Sequence-Directed DNA Binding  
; Molecules, Compositions and Methods

NUMBER OF SEQUENCES: 664

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive

CITY: Redwood City

STATE: CA

COUNTRY: USA

ZIP: 94063

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/993,346

FILING DATE: 13-NO. US20030124530A1-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/354,947

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/171,389

FILING DATE: 20-DEC-1993

APPLICATION NUMBER: US 08/123,936

FILING DATE: 17-SEP-1993

APPLICATION NUMBER: US 07/996,783

FILING DATE: 23-DEC-1992

APPLICATION NUMBER: US 07/723,618

FILING DATE: 27-JUN-1991

APPLICATION NUMBER: US 08/081,070

FILING DATE: 22-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAMS: Brady, John F.

REGISTRATION NUMBER: 39,118

REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 324-0880

TELEFAX: (650) 324-0960

INFORMATION FOR SEQ ID NO: 463:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOMATE: Human insulin-like growth factor II

gene

SEQUENCE DESCRIPTION: SEQ ID NO: 463:

US-09-993-346-463

## Query Match

Best Local Similarity 3.0%; Score 20; DB 10; Length 50;

Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

## QY

259 GGGGGCACACACACCTGCTCCAGCAGGCTTCGGCTGCCGCC 302

## Db

49 GGGGGGGCCACGCGCGGCTCTTATATCGGGCCAGCGCGGCC 6

## RESULT 3

US-10-131-827-677

; Sequence 677, Application US/10131827

; Publication No. US20040009479A1

; GENERAL INFORMATION:

; APPLICANT: Wohlgenuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUN

; FILE REFERENCE: 506612000120

; CURRENT APPLICATION NUMBER: US/10/131,827

; PRIOR FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 10/006,290

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/296,764

; PRIOR FILING DATE: 2001-06-08

; NUMBER OF SEQ ID NOS: 9090

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 677

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-131-827-677

Query Match

Best Local Similarity 3.0%; Score 20; DB 15; Length 50;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

## QY

172 GCCTGCTGCGGAAGACTGCAGAGAAG 199

## Db

16 GCCTGCTGCGGAAGACTGCAGAGAAG 43

## RESULT 4

US-10-319-315-56

; Sequence 56, Application US/10319315

; Publication No. US20030219774A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: NOVEL HUMAN NEUROTRANSMITTER TRANSPORTER

; FILE REFERENCE: D0205 NP

; CURRENT APPLICATION NUMBER: US/10/319,315

; CURRENT FILING DATE: 2002-12-13

; NUMBER OF SEQ ID NOS: 135

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 56

; LENGTH: 42

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-319-315-56

Query Match

Best Local Similarity 2.9%; Score 19.8; DB 15; Length 42;

Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

## QY

23 CTCCTACTTGCACCATCCGCTGACAGTCACAGTGGCC 61

## Db

3 CCCAAGCTTGCACCATCCGGAAGAACAGCAAAATGACC 41

## RESULT 5

US-10-011-931-8/c

; Sequence 8, Application US/10011931

; Publication No. US20030026806A1

; GENERAL INFORMATION:

; APPLICANT: WITTE, ALISON

; APPLICANT: VARNUM, BRIAN C.

; APPLICANT: QIAN, ZUEMING

; APPLICANT: VEZINA, CHRIS

; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BI

; FILE REFERENCE: A-731

; CURRENT APPLICATION NUMBER: US/10/011,931



APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CPI  
CURRENT APPLICATION NUMBER: US/10/349,143  
CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/09/422,978  
PRIOR FILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 2676

LENGTH: 47  
TYPE: DNA

ORGANISM: Homo Sapiens  
FEATURE:

NAME/KEY: allele  
LOCATION: 24

OTHER INFORMATION: 99-13864-64 : polymorphic base G or T  
US-10-349-143-2676

Query Match 2.9%; Score 19.2; DB 15; Length 47;  
Best Local Similarity 70.6%; Pred. No. 4.7e+04;

Matches 24; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 272 CCCTGCTCCAGCAGCTCTCCGGTGGCCCTGC 305

DB 10 CCCTCTCCACAGKCTCCCTCTCCCTCTGC 43

RESULT 10  
US-10-131-827-1287

Sequence 1287, Application US/10131827  
Publication No. US20040009479A1

GENERAL INFORMATION:  
APPLICANT: Wohlgemuth, Jay

APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert

APPLICANT: Ly, Ngoc  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

FILE REFERENCE: 0219s310 - protein C  
CURRENT APPLICATION NUMBER: US/05/978,917A

CURRENT FILING DATE: 2001-10-17  
NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 23

LENGTH: 50  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-978-917A-23

Query Match 2.8%; Score 18.8; DB 10; Length 50;  
Best Local Similarity 63.0%; Pred. No. 6.3e+04;

Matches 29; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 465 CCGGTGGGGTGGAGCTGCGCCATCTCAACGAGCTCAGTCCCG 510

DB 1 CCCTGCGAGTGGTCTGCTGCACTCAACCAAGAGCTGCGCTGC 46

RESULT 13  
US-10-138-195-31

Sequence 31, Application US/10138195  
Publication No. US20030207340A1

GENERAL INFORMATION:  
APPLICANT: Morre, D. James

APPLICANT: Morre, Dorothy J.  
APPLICANT: Chueh, Pin-ju

TITLE OF INVENTION: Sequences Encoding Human Neoplastic Marker  
FILE REFERENCE: 85-99

CURRENT APPLICATION NUMBER: US/10/138,195  
CURRENT FILING DATE: 2002-05-01

Query Match 2.9%; Score 19.2; DB 15; Length 50;  
Best Local Similarity 67.5%; Pred. No. 4.7e+04;

Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 67 AGTTTCCTGGGTCCAGCCCTCTCCAGAGTGGAGCGCG 106

DB 11 AGTCCCTGTGCTCTCAGCCATCCCAAGAGGTTTGCTG 50

RESULT 11  
US-10-131-827-1362/c

Sequence 1362, Application US/10131827

Publication No. US20040009479A1  
GENERAL INFORMATION:  
APPLICANT: Wohlgemuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUN

FILE REFERENCE: 506612000120  
CURRENT APPLICATION NUMBER: US/10/131,827

CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: US 10/006,290

PRIOR FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US 60/296,764

PRIOR FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 9090

SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1362

LENGTH: 50  
TYPE: DNA

ORGANISM: Homo sapiens  
US-10-131-827-1362

Query Match 2.9%; Score 19.2; DB 15; Length 50;  
Best Local Similarity 67.5%; Pred. No. 4.7e+04;

Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 178 CATGGGAAGACTGAGAGAGCTGTGGAGCAACTTGGTG 217

DB 42 CAGTGGGAAGATGCAAGAAAGCTTTAGAGACATAGATG 3

RESULT 12  
US-09-978-917A-23

Sequence 23, Application US/09978917A  
Publication No. US20030027299A1

GENERAL INFORMATION:  
APPLICANT: Maxygen Aps; Maxygen Holdings

TITLE OF INVENTION: Protein C or activated protein C-like molecules  
FILE REFERENCE: 0219s310 - protein C

CURRENT APPLICATION NUMBER: US/05/978,917A  
CURRENT FILING DATE: 2001-10-17

NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 23  
LENGTH: 50

TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-978-917A-23  
Query Match 2.8%; Score 18.8; DB 10; Length 50;  
Best Local Similarity 63.0%; Pred. No. 6.3e+04;

Matches 29; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 465 CCGGTGGGGTGGAGCTGCGCCATCTCAACGAGCTCAGTCCCG 510

DB 1 CCCTGCGAGTGGTCTGCTGCACTCAACCAAGAGCTGCGCTGC 46

RESULT 13  
US-10-138-195-31

Sequence 31, Application US/10138195  
Publication No. US20030207340A1

GENERAL INFORMATION:  
APPLICANT: Morre, D. James

APPLICANT: Morre, Dorothy J.  
APPLICANT: Chueh, Pin-ju

TITLE OF INVENTION: Sequences Encoding Human Neoplastic Marker  
FILE REFERENCE: 85-99

CURRENT APPLICATION NUMBER: US/10/138,195  
CURRENT FILING DATE: 2002-05-01

; PRIOR APPLICATION NUMBER: US 60/162,644  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: PCT US00/30190  
; PRIOR FILING DATE: 2000-11-01  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide  
; OTHER INFORMATION: useful as primer, for example.  
US-10-138-195-31

Query Match 2.8%; Score 18.6; DB 15; Length 38;  
Best Local Similarity 72.7%; Pred. No. 6.7e+04;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
Qy 358 CAGGATCTAATTGGAGATTGGCCAGTTTGGCA 390  
Db 1 CAGGAATGACTGGAGTTGTGGCCAGCCTGGAA 33

RESULT 14  
US-10-138-195-32/c  
; Sequence 32, Application US/10138195  
; Publication No. US20030207340A1  
; GENERAL INFORMATION:  
; APPLICANT: Morre, D. James  
; APPLICANT: Morre, Dorothy J.  
; APPLICANT: Chueh, Pin-Ju  
; TITLE OF INVENTION: Sequences Encoding Human Neoplastic Marker  
; FILE REFERENCE: 85-99  
; CURRENT APPLICATION NUMBER: US/10/138,195  
; PRIOR FILING DATE: 2002-05-01  
; PRIOR APPLICATION NUMBER: US 60/162,644  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: PCT US00/30190  
; PRIOR FILING DATE: 2000-11-01  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide  
; OTHER INFORMATION: useful as primer, for example.  
US-10-138-195-32

Query Match 2.8%; Score 18.6; DB 15; Length 38;  
Best Local Similarity 72.7%; Pred. No. 6.7e+04;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
Qy 358 CAGGATCTAATTGGAGATTGGCCAGTTTGGCA 390  
Db 38 CAGGAATGACTGGAGTTGTGGCCAGCCTGGAA 6

RESULT 15  
US-10-176-255-15  
; Sequence 15, Application US/10176255  
; Publication No. US20030153004A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Russo, Joseph F.  
; APPLICANT: Thomsen, William J.  
; TITLE OF INVENTION: No. US20030153004A1-Endogenous, Constitutively Activated Human Se  
; TITLE OF INVENTION: Small Molecule Modulators Thereof  
; FILE REFERENCE: AREN-0328

; CURRENT APPLICATION NUMBER: US/10/176,255  
; CURRENT FILING DATE: 2002-06-19  
; PRIOR APPLICATION NUMBER: 09/060,188  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: 09/767,013  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 09/292,072  
; PRIOR FILING DATE: 1999-04-14  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 15  
; LENGTH: 43  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-10-176-255-15

Query Match 2.8%; Score 18.6; DB 14; Length 43;  
Best Local Similarity 65.9%; Pred. No. 6.9e+04;  
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
Qy 391 TTGGAGTCAACGCCCTCTTCTCGACTCTGTAGCCCAACA 431  
Db 1 TTCAGCAGTCAACCCACTAGTCTATCTCTGTCAACAAAA 41

Search completed: February 29, 2004, 14:51:49  
Job time : 270.801 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 10:05:33 ; Search time 2724.97 Seconds  
(without alignments)  
10688.739 Million cell updates/sec

Title: US-09-904-568-1\_COPY\_132\_803  
Perfect score: 672  
Sequence: 1 atgtctgcttttgggggctgc.....gtgagcgcaactgcaggac 672

Scoring table:  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 1603530

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

1: gb.ba:\*

2: gb.htg:\*

3: gb.in:\*

4: gb.em:\*

5: gb.ov:\*

6: gb.pat:\*

7: gb.ph:\*

8: gb.pl:\*

9: gb.pr:\*

10: gb.ro:\*

11: gb.sts:\*

12: gb.sy:\*

13: gb.un:\*

14: gb.vi:\*

15: em.ba:\*

16: em.fun:\*

17: em.hum:\*

18: em.in:\*

19: em.imu:\*

20: em.om:\*

21: em.or:\*

22: em.ov:\*

23: em.pat:\*

24: em.ph:\*

25: em.pl:\*

26: em.ro:\*

27: em.sts:\*

28: em.un:\*

29: em.vi:\*

30: em.htg\_hum:\*

31: em.htg\_inv:\*

32: em.htg\_other:\*

33: em.htg\_mus:\*

34: em.htg\_pln:\*

35: em.htg\_rnd:\*

36: em.htg\_man:\*

37: em.htg\_vrt:\*

38: em\_sy:\*

39: em\_htgo\_hum:\*

40: em\_htgo\_mus:\*

41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	21.8	3.2	49	6	AX404880	AX404880 Sequence
C 2	21.4	3.2	50	6	BD174394	BD174394 Cell usef
C 3	21.2	3.2	47	6	AR284756	AR284756 Sequence
C 4	21	3.1	40	6	E14011	E14011 Probe 7/19
C 5	20.8	3.1	42	6	AX710949	AX710949 Sequence
C 6	20.8	3.1	42	6	BD001090	BD001090 Method an
C 7	20.8	3.1	42	6	BD001519	BD001519 Method an
C 8	20.6	3.1	41	6	AX514286	AX514286 Sequence
C 9	20.6	3.1	41	6	AX520468	AX520468 Sequence
C 10	20.6	3.1	47	6	AR284587	AR284587 Sequence
C 11	20.2	3.0	35	6	E22807	E22807 Method for
C 12	20.2	3.0	35	6	AR203329	AR203329 Sequence
C 13	20	3.0	50	6	AR032851	AR032851 Sequence
C 14	20	3.0	50	6	I29591	I29591 Sequence 46
C 15	20	3.0	50	6	I91265	I91265 Sequence 46
C 16	20	3.0	50	6	AR209515	AR209515 Sequence
C 17	20	3.0	50	8	AJ600712	AJ600712 Arabidops
C 18	19.8	2.9	46	6	AR157914	AR157914 Sequence
C 19	19.4	2.9	50	6	AX199530	AX199530 Sequence
C 20	19.2	2.9	32	6	BD061703	BD061703 Antigenic
C 21	19.2	2.9	44	6	AR149584	AR149584 Sequence
C 22	19.2	2.9	47	6	AR290941	AR290941 Sequence
C 23	19	2.8	27	6	AR089960	AR089960 Sequence
C 24	19	2.8	27	6	AR196995	AR196995 Sequence
C 25	19	2.8	27	6	AR259149	AR259149 Sequence
C 26	18.8	2.8	42	6	AX080016	AX080016 Sequence
C 27	18.8	2.8	43	6	AX466471	AX466471 Sequence
C 28	18.8	2.8	48	10	S77040	S77040 T-cell rece
C 29	18.8	2.8	50	6	BD225137	BD225137 Polymorph
C 30	18.6	2.8	43	6	AR107092	AR107092 Sequence
C 31	18.6	2.8	43	6	AR111855	AR111855 Sequence
C 32	18.6	2.8	43	6	AR118372	AR118372 Sequence
C 33	18.6	2.8	43	6	AR302214	AR302214 Sequence
C 34	18.6	2.8	43	6	AX813374	AX813374 Sequence
C 35	18.6	2.8	43	6	BD132482	BD132482 Binding m
C 36	18.6	2.8	47	6	AX236856	AX236856 Sequence
C 37	18.4	2.7	31	6	AX286510	AX286510 Sequence
C 38	18.4	2.7	37	6	AR012326	AR012326 Sequence
C 39	18.4	2.7	37	6	AR012348	AR012348 Sequence
C 40	18.4	2.7	39	6	BD065047	BD065047 Hematopoi
C 41	18.4	2.7	39	6	E49257	E49257 Omega 3 fat
C 42	18.4	2.7	40	6	AX538550	AX538550 Sequence
C 43	18.4	2.7	47	6	I77232	I77232 Sequence 22
C 44	18.4	2.7	48	6	AX582839	AX582839 Sequence
C 45	18.4	2.7	50	6	AR252548	AR252548 Sequence

ALIGNMENTS

RESULT 1	AX404880/C	AX404880	Sequence 13 from Patent WO0222833.	49 bp	DNA	linear	PAT 14-JUN-2002
LOCUS	AX404880	AX404880	Sequence 13 from Patent WO0222833.				
DEFINITION	AX404880	AX404880	Sequence 13 from Patent WO0222833.				
ACCESSION	AX404880	AX404880	Sequence 13 from Patent WO0222833.				
VERSION	AX404880.1	AX404880.1	GI:21438112				
KEYWORDS			synthetic construct				
SOURCE			synthetic construct				
ORGANISM			artificial sequences.				
REFERENCE							
AUTHORS			Pfizenmaier,K., Wuest,T., Moosmayer,D., Grell,M. and Scheurich,P.				
TITLE			Fusion protein from antibody cytokine-cytokine inhibitor				
			(selectokine) for use as target-specific prodrug				
JOURNAL			Patent: WO 0222833-A 13 21-MAR-2002;				

Universitaet Stuttgart (DE) ; Pfizenmaier, Klaus (DE)  
AUTHORS  
TITLE Location/Qualifiers  
FEATURES  
source  
1. .49  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer 4 fuer die Amplifikation eines humanen  
TNF-Fragments"

ORIGIN  
Query Match 3.2%; Score 21.8; DB 6; Length 49;  
Best Local Similarity 70.7%; Pred. No. 8.1e+05;  
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 74 TGGGTTCCAGCCCTCTCCAGAGTGACGGCGGTGCTCAG 114  
|||||  
Db 46 TGGGATCATGCCCTGTCCGGATCGAGGTCGTGATCCG 6

RESULT 2  
BD174394  
LOCUS 50 bp DNA linear PAT 18-MAR-2003  
DEFINITION  
Cell useful for evaluation of action of sex hormone receptor.  
ACCESSION  
BD174394  
VERSION  
BD174394.1 GI:29120078  
KEYWORDS  
JP 2002247986-A/27.  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.  
REFERENCE  
1 (bases 1 to 50)  
AUTHORS  
Nakao, T., Matsue, K. and Takebayashi, N.  
TITLE  
Cell useful for evaluation of action of sex hormone receptor  
JOURNAL  
Patent: JP 200247986-A 27 03-SEP-2002;  
MITSUI CHEMICALS INC  
COMMENT  
OS Artificial Sequence  
PN JP 2002247986-A/27  
PD 03-SEP-2002  
PF 23-FEB-2001 JP 2001048876  
PI TOSHIFUMI NAKAO, KAORI MATSUE, NOZOMI TAKEBAYASHI PC  
C12N15/09, C12N5/10, C12Q1/66, C12Q1/66, C12N5/10, C12R1/91, PC  
(C12Q1/02, C12R1/91), (C12Q1/66, C12R1/91), C12N15/00, C12N5/00, PC  
(C12N5/00, C12R1/91)  
CC Description of Artificial Sequence: Primer  
FH Key Location/Qualifiers  
FT source 1. .50  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Query Match 3.2%; Score 21.4; DB 6; Length 50;  
Best Local Similarity 66.0%; Pred. No. 1e+06;  
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 136 AGCAGCTTCAGAAAGTTCTTGAATCTTAGTCGGGCGCTGCTGG 182  
|||||  
Db 4 AGCTTCTCGGCACGCTGTGACGCTGTAAAGCGGGTCTGTCAGGG 50

RESULT 3  
AR284756/c  
LOCUS 47 bp DNA linear PAT 10-APR-2003  
DEFINITION  
Sequence 808 from patent US 6528260.  
ACCESSION  
AR284756  
VERSION  
AR284756.1 GI:29721660  
KEYWORDS  
Unknown.  
SOURCE  
Unknown.  
ORGANISM  
Unclassified.  
REFERENCE  
1 (bases 1 to 47)

Blumenfeld, M., Chumakov, I., Bougueleret, L. and Cohen, A.  
AUTHORS  
TITLE Biallelic markers related to genes involved in drug metabolism  
JOURNAL Patent: US 6528260-A 808 04-MAR-2003;  
FEATURES  
Location/Qualifiers  
source  
1. .47  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 3.2%; Score 21.2; DB 6; Length 47;  
Best Local Similarity 65.9%; Pred. No. 1.2e+06;  
Matches 29; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 96 AGTGAGCGCGCTGCTCAGCTCTTGAGGACTTAGACAGGCA 139  
|||||  
Db 44 AGCGATGCCCTTGGGCGAGAKTTGGAGGGAAGGGGACAGGCA 1

RESULT 4  
E14011  
LOCUS 40 bp DNA linear PAT 28-JUL-1999  
DEFINITION  
Probe.  
ACCESSION  
E14011  
VERSION  
E14011.1 GI:5708694  
KEYWORDS  
JP 1997257798-A/1.  
SOURCE  
unidentified  
ORGANISM  
unclassified.  
REFERENCE  
1 (bases 1 to 40)  
AUTHORS  
Shimada, K. and Namatame, Y.  
TITLE  
IMMOBILIZATION OF GENE  
JOURNAL Patent: JP 1997257798-A 1 03-OCT-1997;  
SUMITOMO METAL IND LTD  
COMMENT  
OS None  
OC Artificial sequences.  
PN JP 1997257798-A/1  
PD 03-OCT-1997  
PF 19-MAR-1996 JP 1996062885  
PI SHIMADA KAZUNORI, NAMATAME YASUKO  
PC G01N33/566, C12N15/09, C12Q1/68;  
CC strandedness: Single;  
CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No;  
FH Key Location/Qualifiers  
FT source 1. .40  
/organism="Artificial sequences".  
/organism="unidentified"  
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/db\_xref="taxon:32644"

ORIGIN  
Query Match 3.1%; Score 21; DB 6; Length 40;  
Best Local Similarity 73.0%; Pred. No. 1.3e+06;  
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 308 GTCTAAAGCCAGATGCTTCCAGGAAGAGCTCCAGGA 344  
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Db 4 GTCTCAGCTCATGCTTTCAGGTAGAGCTCTTGA 40

RESULT 5  
AX710949  
LOCUS 42 bp RNA linear PAT 11-APR-2003  
DEFINITION  
Sequence 249 from Patent EP1288296.  
ACCESSION  
AX710949  
VERSION  
AX710949.1 GI:29787330  
KEYWORDS  
Human herpesvirus 5  
SOURCE  
Human herpesvirus 5  
ORGANISM

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
Betaherpesvirinae; Cytomegalovirus.

REFERENCE  
AUTHORS

Draper, K.G., McSwiggen, J.A., Holecek, J.J., Dudycz, L.W.,  
Macejak, D.G., and Mamone, J.A.

Method and reagent for inhibiting HBV viral replication

Patent: JP 2000342285-A 249 05-MAR-2003;

RIBOZYME PHARMACEUTICALS, INC. (US)

Location/Qualifiers

1. .42

/organism="Human herpesvirus 5"

/mol\_type="unassigned RNA"

/db\_xref="taxon:10359"

## ORIGIN

Query Match 3.1%; Score 20.8; DB 6; Length 42;

Best Local Similarity 70.0%; Pred. No. 1.5e+06;

Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 201 TGTGGAGCACTTGTGCGCGCCACCTGTCTCAGAGAG 240

Db 2 TGTGGATGACCTACGGGCCATCGCGGAGGAGTCAGATGAG 41

## RESULT 6

BD001090

LOCUS

DEFINITION Method and reagent for inhibiting viral replication.

ACCESSION BD001090

VERSION BD001090.1 GI:18625649

KEYWORDS JP 2000342285-A/250.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 42)

AUTHORS Draper, K.G., Dadykztz, L.W., Macswigen, J.A., Maysejak, D.G.,  
Holesek, J.J., and Mamone, A.J.

TITLE Method and reagent for inhibiting viral replication

JOURNAL Patent: JP 2000342285-A 250 12-DEC-2000;

RIBOZYME PHARMACEUTICALS INC

OS Artificial Sequence

PN JP 2000342285-A/250

PD 12-DEC-2000

PF 01-MAY-2000 JP 2000132616

PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR

14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR

14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR

14-MAY-1992 US 07/882866, 14-MAY-1992 US 07/882868 PR

14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882891 PR

14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/882923 PR

14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR

14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR

14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR

31-JUL-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR

26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR

15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR

07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI

KENNETH G DRAPER, LEC W DADYKTZ, JAMES A MACSWIGEN, PI DENNIS G

MAYSEJAK.

PI JAMES J HOLESEK, ANTHONY J MAMONE

PC C12N15/09, C12N5/10, C12N7/00, C12N9/22, C12N15/10, C12R1:91, PC

C12N15/00,

PC C12N5/00, C12N5/00, C12R1:91)

CC C12N5/00, C12N5/00, C12R1:91)

PH Key Location/Qualifiers

FT source 1. .42

FT Location/Qualifiers

FT Location/Qualifiers

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FT Location/Qualifiers

## ORIGIN

Query Match 3.1%; Score 20.8; DB 6; Length 42;

Best Local Similarity 70.0%; Pred. No. 1.5e+06;

Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 201 TGTGGAGCACTTGTGCGCGCCACCTGTCTCAGAGAG 240

Db 2 TGTGGATGACCTACGGGCCATCGCGGAGGAGTCAGATGAG 41

## RESULT 7

BD001519

LOCUS

DEFINITION Method and reagent for inhibiting viral replication.

ACCESSION BD001519

VERSION BD001519.1 GI:18626078

KEYWORDS JP 2000342286-A/250.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 42)

AUTHORS Draper, K.G., Dadykztz, L.W., Macswigen, J.A., Maysejak, D.G.,  
Holesek, J.J., and Mamone, A.J.

TITLE Method and reagent for inhibiting viral replication

JOURNAL Patent: JP 2000342286-A 250 12-DEC-2000;

RIBOZYME PHARMACEUTICALS INC

OS Artificial Sequence

PN JP 2000342286-A/250

PD 12-DEC-2000

PF 01-MAY-2000 JP 2000132651

PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR

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14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR

14-MAY-1992 US 07/882866, 14-MAY-1992 US 07/882868 PR

14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882891 PR

14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/882923 PR

14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR

14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR

14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR

31-JUL-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR

26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR

15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR

07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI

KENNETH G DRAPER, LEC W DADYKTZ, JAMES A MACSWIGEN, PI DENNIS G

MAYSEJAK,

PI JAMES J HOLESEK, ANTHONY J MAMONE

PC C12N15/09, C12N5/10, C12N7/00, C12N9/22, C12N15/10, C12R1:91, PC

PC A61K39/135,

PC A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,

PC A61P1/16,

PC A61P1/14, A61P1/16, A61P1/18, A61P1/22, A61P35/02, C12O1/68, PC

C12N15/09, C12R1:93, C12N15/00, C12N5/00, A61K37/48, C12N15/00, PC

C12R1:93)

CC C12N15/09, C12N5/00, C12R1:93)

PH Key Location/Qualifiers

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FT Location/Qualifiers

FT Location/Qualifiers

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FT Location/Qualifiers

FT Location/Qualifiers

FT Location/Qualifiers

RESULT 8  
AX514286/c  
LOCUS AX514286 41 bp DNA linear PAT 05-OCT-2002  
DEFINITION Sequence 484 from Patent WO02052044.  
ACCESSION AX514286  
VERSION AX514286.1 GI:23560673  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
AUTHORS Detection of genetic polymorphisms  
TITLE Patent: WO 02052044-A 484 04-JUL-2002;  
JOURNAL Riken (JP)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
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Best Local Similarity 70.3%; Pred. No. 1.7e+06;  
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;  
QY 20 CAGCTCCATCTGACCATCCGCTGACAGTCACAG 56  
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Db 38 CAGCCCTGTAACGACATCTGCTGAGGCTCTCGG 2  
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RESULT 9  
AX520468/c  
LOCUS AX520468 41 bp DNA linear PAT 05-OCT-2002  
DEFINITION Sequence 6666 from Patent WO02052044.  
ACCESSION AX520468  
VERSION AX520468.1 GI:23571065  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
AUTHORS Detection of genetic polymorphisms  
TITLE Patent: WO 02052044-A 6666 04-JUL-2002;  
JOURNAL Riken (JP)  
FEATURES  
source Location/Qualifiers  
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Best Local Similarity 70.3%; Pred. No. 1.7e+06;  
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Db 38 CAGCCCTGTAACGACATCTGCTGAGGCTCTCGG 2  
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RESULT 10  
AR284587  
LOCUS AR284587 47 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 639 from patent US 6528260.  
ACCESSION AR284587  
VERSION AR284587.1 GI:29721491  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 47)  
AUTHORS Blumenfeld, M., Chumakov, I., Bougueleret, L. and Cohen, A.  
TITLE Biallelic markers related to genes involved in drug metabolism  
JOURNAL Patent: US 6528260-A 639 04-MAR-2003;  
FEATURES  
source Location/Qualifiers  
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Query Match 3.1%; Score 20.6; DB 6; Length 47;  
Best Local Similarity 64.4%; Pred. No. 1.7e+06;  
Matches 29; Conservative 1; Mismatches 15; Indels 0; Gaps 0;  
QY 596 AGCTGGGTACAGTGTAGCCTTGGTCCTTAAGGAGATGGCAGAAC 640  
|||||  
Db 3 AGGTAGGGACAGTGAAGCATKGGGGGGCCAGGAGCTCCAGAGC 47  
|||||  
RESULT 11  
E22807  
LOCUS E22807 35 bp DNA linear PAT 18-JUN-2001  
DEFINITION Method for screening PPAR agonist and antagonist.  
ACCESSION E22807  
VERSION E22807.1 GI:13024121  
KEYWORDS JP 1999056369-A/2.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Junko, M. and Tomoyasu, T.  
TITLE Method for screening PPAR agonist and antagonist  
JOURNAL Patent: JP 1999056369-A 2 02-MAR-1999;  
TANABE SEIYAKU CO LTD  
COMMENT OS Unidentified  
PN JP 1999056369-A/2  
PD 02-MAR-1999  
PF 27-AUG-1997 JP 1997231084  
PR JUNKO MINAKAMI, TOMOYASU TANIGUCHI  
PI C12N15/09; C12N1/19, C12Q1/68// (C12N1/19, C12R1/645), C12N15/00 CC  
PC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
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Best Local Similarity 75.8%; Pred. No. 2.2e+06;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 86 CCTCTCCAGAGTGACGGCGCTGGCTCAGCTCT 118  
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Db 1 CCGCTCGAGAAATGTTGGCAGTGGCTCAGGACT 33  
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RESULT 12  
AR203329  
LOCUS AR203329 35 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 2 from patent US 6365361.  
ACCESSION AR203329  
VERSION AR203329.1 GI:21499690  
KEYWORDS  
SOURCE Unknown.



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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35)
AUTHORS Taniguchi, T. and Mizukami, J.
TITLE Method for identifying or screening agonist and antagonist to PPAR
JOURNAL Patent: US 6365361-A 2 02-APR-2002;
FEATURES
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Qy 86 CCTCTCCAGAGTGACGCGCGCTGCTCAGCTCT 118
Db 1 CCGCTCGAGAAATGTTGGCAGTGGCTCAGGACT 33
RESULT 13
LOCUS AR032851/c
DEFINITION Sequence 463 from patent US 5869241.
ACCESSION AR032851
VERSION AR032851.1 GI:5948456
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E.
TITLE Method of determining DNA sequence preference of a DNA-binding molecule
JOURNAL Patent: US 5869241-A 463 09-FEB-1999;
FEATURES
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    Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Qy 259 GCGGGCACACACACCTGCTCCAGCAGGCTCTCGGCTGCCCC 302
Db 49 GCGGGGCGCCACCGCGGCTCTTATAGTCGCCCGCCGCGGCC 6
RESULT 14
LOCUS I29591/c
DEFINITION Sequence 463 from patent US 5578444.
ACCESSION I29591
VERSION I29591.1 GI:1820382
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E.
TITLE Sequence-directed DNA-binding molecules compositions and methods
JOURNAL Patent: US 5578444-A 463 26-NOV-1996;
FEATURES
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        /mol_type="unassigned DNA"
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    Best Local Similarity 65.9%; Pred. No. 2.4e+06;
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Qy 259 GCGGGCACACACACCTGCTCCAGCAGGCTCTCGGCTGCCCC 302
Db 49 GCGGGGCGCCACCGCGGCTCTTATAGTCGCCCGCCGCGGCC 6
MATCHES 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Qy 259 GCGGGCACACACACCTGCTCCAGCAGGCTCTCGGCTGCCCC 302
Db 49 GCGGGGCGCCACCGCGGCTCTTATAGTCGCCCGCCGCGGCC 6
RESULT 15
LOCUS I91265/c
DEFINITION Sequence 463 from patent US 5726014.
ACCESSION I91265
VERSION I91265.1 GI:3935735
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Edwards, C.A., Cantor, C.R., Andrews, B.M. and Turin, L.M.
TITLE Screening assay for the detection of DNA-binding molecules
JOURNAL Patent: US 5726014-A 463 10-MAR-1998;
FEATURES
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        /mol_type="unassigned DNA"
ORIGIN
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Db 49 GCGGGGCGCCACCGCGGCTCTTATAGTCGCCCGCCGCGGCC 6
MATCHES 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 10:34:43 ; Search time 2031.49 Seconds  
(without alignments)  
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Title: US-09-904-568-1\_COPY\_132\_803

Perfect score: 672

Sequence: 1 atgtctgcttgggggtgc.....gtgagcgcaactgcaggac 672

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 138346

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	3.3	50	9	AU106355
C 2	20.6	3.1	50	9	AU104945
C 3	20.4	3.0	40	9	AA933650
C 4	20.4	3.0	49	28	AZ971265

C	5	20.4	3.0	50	9	AU106354
C	6	19.8	2.9	50	9	AU104331
C	7	19.6	2.9	47	29	AL757838
C	8	19.4	2.9	41	12	BI669410
C	9	19.4	2.9	47	12	BI544737
C	10	19.4	2.9	50	9	AU106356
C	11	19.4	2.9	50	12	BG314884
C	12	19.2	2.9	50	9	AU104702
C	13	19	2.8	42	28	AQ025866
C	14	19	2.8	50	28	AZ479659
C	15	18.8	2.8	50	9	AU106353
C	16	18.8	2.8	50	9	AU107055
C	17	18.8	2.8	50	9	AU107064
C	18	18.6	2.8	50	9	AU103136
C	19	18.4	2.7	40	28	AZ666390
C	20	18.4	2.7	42	12	BJ063892
C	21	18.4	2.7	44	12	BM400948
C	22	18.4	2.7	45	12	BM397151
C	23	18.4	2.7	49	9	AA280723
C	24	18.4	2.7	50	29	CG720601
C	25	18.2	2.7	40	12	BI825771
C	26	18.2	2.7	43	9	AA116340
C	27	18.2	2.7	46	9	AA052407
C	28	18.2	2.7	48	29	CG802067
C	29	18.2	2.7	50	9	AU103070
C	30	18.2	2.7	50	9	AU104084
C	31	18	2.7	43	12	BJ001433
C	32	18	2.7	45	28	BZ585215
C	33	18	2.7	47	9	AV833049
C	34	18	2.7	47	28	AZ778260
C	35	18	2.7	47	28	BZ596680
C	36	18	2.7	50	9	AU102993
C	37	18	2.7	50	9	AU103858
C	38	18	2.7	50	9	AU103860
C	39	18	2.7	50	9	AU103898
C	40	18	2.7	50	9	AU104250
C	41	18	2.7	50	9	AU105404
C	42	18	2.7	50	9	AU107645
C	43	18	2.7	50	9	AU107646
C	44	17.8	2.6	38	28	AQ025526
C	45	17.8	2.6	41	12	BG390320

#### ALIGNMENTS

RESULT 1	AU106355/c	AU106355	50 bp	mrna	linear	EST 30-AUG-2001
LOCUS	AU106355	Sugano Homo sapiens cdna library Homo sapiens cdna clone				
DEFINITION	KAT02155, mRNA sequence.					
ACCESSION	AU106355					
VERSION	AU106355.1	GI:13555876				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 50)					
AUTHORS	Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.					
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites					
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)					
MEDLINE	21270072					
PUBMED	11375929					
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and					

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

## FEATURES

source Location/Qualifiers

1..50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="KAT02155"  
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## ORIGIN

Query Match 3.3%; Score 22; DB 9; Length 50;  
Best Local Similarity 73.7%; Pred. No. 3e+05;  
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 264 CACACACCCGCTCCAGCAGCTCCGGTGGCCCC 301  
|||||  
DB 50 CCCACGACCCAGCAGCTCCGGCTCCAGCGCCCC 13

## RESULT 2

AU104945/c  
LOCUS AU104945 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION HRC05721, mRNA sequence.

ACCESSION AU104945

VERSION AU104945

KEYWORDS EST.

SOURCE AU104945.1 GI:13554466

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 50)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
Rata, H., Oca, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

PUBMED 11375929

CONTACT: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997).

## FEATURES

source Location/Qualifiers

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/organism="Homo sapiens"  
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/clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

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Best Local Similarity 74.3%; Pred. No. 6.6e+05;  
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 270 CACCTGCTCCAGCAGCTCTCGGCTGCCCTG 304  
|||||  
DB 45 CACTGCTCCAGCGGCTCCAGCGTGCCTGCTG 11

## RESULT 3

AA933650/c  
LOCUS AA933650 40 bp mRNA linear EST 27-APR-1998  
DEFINITION OT56C06.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA clone IMAGE:1551178 3'

similar to SW:DPD2\_HUMAN P49005 DNA POLYMERASE DELTA SMALL SUBUNIT  
; mRNA sequence.

ACCESSION AA933650

VERSION AA933650.1 GI:3089918

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 40)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Seq primer: -40m13 fwd. BT from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..40

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1551178"

/lab\_host="DH10B"

/tissue\_type="pooled germ cell tumors"

/clone\_lib="NCI\_CGAP GC4"

/notes="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; 1st strand cDNA was prepared from 3 pooled

germ cell tumors, and was then primed with a Not I -

oligo(dT) primer. Double-stranded cDNA was ligated to Eco

RI adaptors (Pharmacia), digested with Not I and cloned

into the Not I and Eco RI sites of the modified pT73

vector. Library is normalized. Library was constructed by

Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 3.0%; Score 20.4; DB 9; Length 40;  
Best Local Similarity 71.1%; Pred. No. 6.5e+05;  
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGTCTGCTTTGGGGCTGCAGCTCCATCTGCACCA 38  
|||||  
DB 39 ATGTCTACTTTTGTGGCACACCCCGCTTGTCTCCA 2

## RESULT 4

AZ971265/c

LOCUS AZ971265

DEFINITION 2M0244N12R Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0244N12 R, genomic survey sequence.

ACCESSION AZ971265

VERSION AZ971265.1 GI:13842492

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 49)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
JOURNAL plasmid inserts  
MEDLINE Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112 USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dgunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0244 row: N column: 12  
Seq primer: CACACAGGAAACAGTATGACC  
Class: plasmid ends  
High quality sequence stop: 49.  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN  
Query Match 3.0%; Score 20.4; DB 28; Length 49;  
Best Local Similarity 71.1%; Pred. No. 7.3e+05;  
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
Qy 252 CTTGCTGCGGCGACACACCTGCTCCAGCAGGCTC 289  
Db 42 CCAGAAGCGCGCACCATGATGCTCTCCAGCAGTCTC 5

RESULT 5  
AUI06354/c  
LOCUS AUI06354 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION COL00924, mRNA sequence.  
ACCESSION AUI06354  
VERSION AUI06354.1 GI:13555875  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)  
Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese.J.,  
Hata.H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Okubo.K.,  
Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano.S.  
Diverse transcriptional initiation revealed by fine, large-scale

TITLE mapping of mRNA start sites  
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
MEDLINE 21270072  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp  
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and  
Sugano.S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997).  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="COLF0073"  
/clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN  
Query Match 2.9%; Score 19.8; DB 9; Length 50;  
Best Local Similarity 77.4%; Pred. No. 1e+06;  
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 264 CACACACACCTGCTCCAGCAGGCTCTCCGCTGCCCC 301  
Db 49 CCACGCCACCAAGACTCCCGCTCTCCAGCGCCCC 12

JOURNAL mapping of mRNA start sites  
MEDLINE EMBO Rep. 2 (5), 388-393 (2001)  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp  
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and  
Sugano.S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997).  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="COLF0073"  
/clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN  
Query Match 3.0%; Score 20.4; DB 9; Length 50;  
Best Local Similarity 71.1%; Pred. No. 7.4e+05;  
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
Qy 264 CACACACACCTGCTCCAGCAGGCTCTCCGCTGCCCC 301  
Db 49 CCACGCCACCAAGACTCCCGCTCTCCAGCGCCCC 12

RESULT 6  
AUI04331  
LOCUS AUI04331 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION COL007073, mRNA sequence.  
ACCESSION AUI04331.1 GI:13553852  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)  
Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese.J.,  
Hata.H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Okubo.K.,  
Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano.S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
21270072  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp  
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and  
Sugano.S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997).  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="COLF0073"  
/clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN  
Query Match 2.9%; Score 19.8; DB 9; Length 50;  
Best Local Similarity 77.4%; Pred. No. 1e+06;  
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 264 CACACACACCTGCTCCAGCAGGCTCTCCGCTGCCCC 301  
Db 49 CCACGCCACCAAGACTCCCGCTCTCCAGCGCCCC 12

QY 629 AGATGGCAGAACTGGAGAGAAAGTGTGAGCG 659  
 Db 20 AGATGGCAGAACTAGAGCAGAGAGAGAGCG 50

RESULT 7  
 AL757838/c  
 LOCUS 47 bp DNA linear GSS 18-JUN-2002  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-152H09-013139, genomic survey sequence.

ACCESSION AL757838  
 VERSION AL757838.1 GI:21496186  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsiis.

REFERENCE 1 Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H. and Weissshaar, B.  
 A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines  
 Unpublished

JOURNAL 2  
 REFERENCE Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weissshaar, B.  
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics  
 Unpublished

JOURNAL 3 (bases 1 to 47)  
 REFERENCE Strizhov, N., Li, Y., Rosso, M. and Weissshaar, B.  
 Direct Submission  
 Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At4g18700. The sequences are generated at the MPI for plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES  
 source  
 1..47  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-152H09-013139"  
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA from insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

ORIGIN  
 Query Match 2.9%; Score 19.6; DB 29; Length 47;  
 Best Local Similarity 73.5%; Pred. NO. 1.1e+06;  
 Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 571 GAGTCCCATACCCAAATTCAGGAGCTCCGGT 604  
 Db 39 GAGGATCCCATAGGTTTGTTCGGAGCTCCGGT 6

RESULT 8  
 BI669410/c

LOCUS BI669410 41 bp mRNA linear EST 12-SEP-2001  
 DEFINITION 603295295F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:5314750 5', mRNA sequence.

ACCESSION BI669410  
 VERSION BI669410.1 GI:15583643  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 41)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs@mail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM11797 row: m column: 23  
 High quality sequence stop: 41.  
 Location/Qualifiers  
 1..41  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5314750"  
 /tissue\_type="hypothalamus"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_96"  
 /note="Organ: Brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 2.9%; Score 19.4; DB 12; Length 41;  
 Best Local Similarity 79.3%; Pred. NO. 1.2e+06;  
 Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 283 CAGGCTCTCCGGCTGCCCTGCTAGTCT 311  
 Db 41 CAAGATGTCGGCCGCCCTGCTGCTCT 13

RESULT 9  
 BI544737/c  
 LOCUS BI544737 47 bp mRNA linear EST 05-SEP-2001  
 DEFINITION 603242001F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5284488 5', mRNA sequence.

ACCESSION BI544737  
 VERSION BI544737.1 GI:15432049  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 47)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.

Email: csapbs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CNA Sequencing by: Incyte Genomics, Inc.

DNA distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L2A111719 row: a column: 01

High quality sequence stop: 47.

Location/Qualifiers

1. .47

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:528488"

/tissue\_type="hippocampus"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_95"

/note="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI

(Gcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTNN-3', size-selected for average

insert size 2.5 kb and normalized to ROT 5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIH/NHGRI, National Institutes of Health). Note: this

is a NIH\_MGC Library."

## ORIGIN

Query Match 2.9%; Score 19.4; DB 12; Length 47;  
Best Local Similarity 79.3%; Pred. No. 1.3e+06;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 283 CAGGCTCTCGGCTGCCCTGCTAGTCT 311

DB 47 CAAGATGTCGCGCGCCCTGCTCT 19

## RESULT 10

AU106356/c

LOCUS

DEFINITION AU106356 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
KAT03974, mRNA sequence.

ACCESSION AU106356

VERSION AU106356.1

KEYWORDS GI:13555877

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Kata, H., Oka, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

11375929

CONTACT: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

Location/Qualifiers

1. .50

## FEATURES

source

## ORIGIN

Query Match 2.9%; Score 19.4; DB 9; Length 50;  
Best Local Similarity 70.3%; Pred. No. 1.3e+06;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 258 GCGCGGCACACACACCCCTGCTCCAGCAGGCTCTCCGG 294

DB 37 GGCAGCCCCACGCACACAGCGACTCCGCGCTCTCCAG 1

## RESULT 11

BG314884

LOCUS

DEFINITION BG314884

OP2.0.138 Human THP1 cell line library Homo sapiens cDNA, mRNA

sequence.

ACCESSION BG314884

VERSION BG314884.1

KEYWORDS GI:18997731

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 50)

Andersson, T., Borang, S., Larsson, M., Thelin, A.,

Ekstrand-Hammarstrom, B., Wirta, V., Wenborg, A., Lundberg, J. and

Odeberg, J.

Identification of candidate genes in atherosclerosis - Virtual chip

analysis in RDA based transcript profiling of monocyte/macrophage

response to oxidised LDL

Unpublished (2001)

CONTACT: Andersson Tove

Department of Biotechnology

KTH

Teknikringen 34, plan 6, 100 44 Stockholm, Sweden

Tel: +46 8 790 71 29

Fax: +46 8 245452

Email: tove@biochem.kth.se

POLYA-No.

Location/Qualifiers

1. .50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/cell\_line="THP1"

/clone\_lib="Human THP1 cell line library"

/note="Vector: pRIT28; Site 1: BamHI; Site 2: BamHI;

Shotgun cloning of RDA difference products - Macrophage and

foamcell libraries were submitted to successive rounds of

subtractive hybridisations generating populations of gene

fragments that are differentially expressed in macrophage

to foam cell formation."

LOCATION/Qualifiers

1. .50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/cell\_line="THP1"

/clone\_lib="Human THP1 cell line library"

/note="Vector: pRIT28; Site 1: BamHI; Site 2: BamHI;

Shotgun cloning of RDA difference products - Macrophage and

foamcell libraries were submitted to successive rounds of

subtractive hybridisations generating populations of gene

fragments that are differentially expressed in macrophage

to foam cell formation."

LOCATION/Qualifiers

1. .50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/cell\_line="THP1"

/clone\_lib="Human THP1 cell line library"

/note="Vector: pRIT28; Site 1: BamHI; Site 2: BamHI;

Shotgun cloning of RDA difference products - Macrophage and

foamcell libraries were submitted to successive rounds of

subtractive hybridisations generating populations of gene

fragments that are differentially expressed in macrophage

ACCESSION AU104702  
 VERSION AU104702.1 GI:13554223  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 50)  
 AUTHORS Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano,J., Sese,J., Hata,H., Oca.T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano,S.  
 TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 MEDLINE 21270072  
 PUBMED 11375929  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki.Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and Characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
 FEATURES source  
 Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="HRC06060"  
 /clone\_lib="Sugano Homo sapiens cDNA library"  
 ORIGIN  
 Query Match 2.9%; Score 19.2; DB 9; Length 50;  
 Best Local Similarity 67.5%; Pred. No. 1.5e+06;  
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
 QY 244 CTGGCGGCTCTGCTGGCGGCACACACACCTGCTCCAGC 283  
 Db 11 CTGGCGGCGCAGCGGGCGGCTCCAGCAGCGCGCTGC 50  
 RESULT 13  
 AQ025866/c  
 LOCUS  
 DEFINITION 42 bp DNA linear GSS 30-JUN-1998  
 1(2)K08708 Drosophila melanogaster P lethal line Drosophila melanogaster genomic sequence recovered from 5' end of P element, genomic survey sequence.  
 ACCESSION AQ025866  
 VERSION AQ025866.1 GI:3266218  
 KEYWORDS GSS.  
 SOURCE Drosophila melanogaster (fruit fly)  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Spradling,A.C., Stern,D., Beaton,A., Rehm,E.J., Laverdy,T., Mozdzen,N., Misra,S. and Rubin,G.M.  
 TITLE The BDGP gene disruption project: Single P element insertions mutating 30% of Drosophila autosomal genes  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Gerald Rubin  
 Berkeley Drosophila Genome Project  
 University of California, Berkeley  
 LSA Building, Berkeley, CA 94720-3200, USA  
 Fax: 5106433947  
 Email: gerry@fruitfly.berkeley.edu  
 Sequence recovery method was inverse PCR.  
 Sequence orientation is forward strand relative to 5' end of P element  
 The P element insertion position is base 035 in the 42 bases. This insertion position refers to the first base of the 8 base target recognition sequence.  
 Class: transposon-tagged.  
 FEATURES source  
 Location/Qualifiers  
 1..42  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone\_lib="Drosophila melanogaster P lethal line"  
 /notes="Inverse PCR was performed on Drosophila melanogaster strains each of which contains a single P transposable element insertion that is thought to cause either lethality or sterility. The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfly.berkeley.edu/p\_disrupt/inverse\_pcr.html."  
 ORIGIN  
 Query Match 2.8%; Score 19; DB 28; Length 42;  
 Best Local Similarity 69.4%; Pred. No. 1.5e+06;  
 Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 QY 21 AGCTCCATCTTCACCATCCCGCTGACAGTCACAG 56  
 Db 36 AGTACTATATGCTCCATNCCGATACCGCCACAG 1  
 RESULT 14  
 AZ479659/c  
 LOCUS  
 DEFINITION 50 bp DNA linear GSS 04-OCT-2000  
 1M0300B03R Mouse 10kb plasmid TUGC1M library Mus musculus genomic clone UUGC1M0300B03 R, genomic survey sequence.  
 ACCESSION AZ479659  
 VERSION AZ479659.1 GI:10639488  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 50)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0300 row: B column: 03  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 50.  
 FEATURES source  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0300B03"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid TUGC1M library"

